

# JOURNAL OF CREATION

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CHANGING RINGS

BLOOD CLOTS IN DINOSAUR  
BONES—EVIDENCE FOR  
FLOOD DEATH?

# Whales —DESIGNED OR EVOLVED?

NEO-DARWINISM CRISIS—  
EXPERTS CALL FOR NEW  
THEORY OF EVOLUTION

PETROLEUM SYSTEMS  
DO NOT REQUIRE  
MILLIONS OF YEARS



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**COVER:** Mother and calf humpback whales

**IMAGE:** drewsulock © Envato Elements

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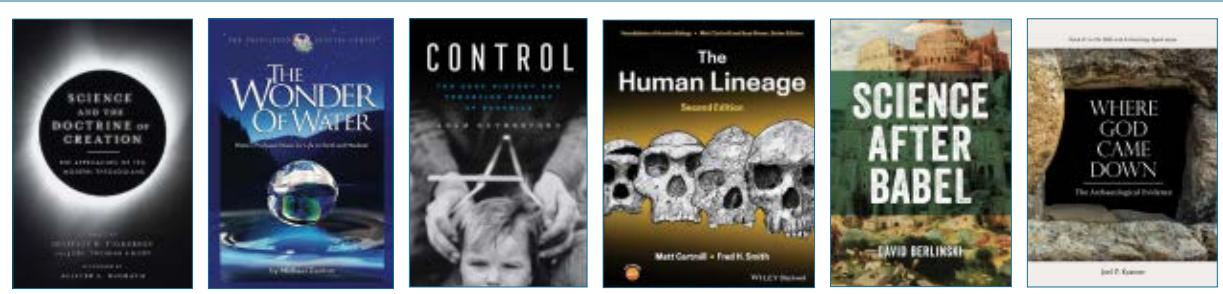
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- » The account of origins presented in Genesis is a simple but factual presentation of actual

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- » Scripture teaches a recent origin for man and the whole creation.
- » The great Flood of Genesis was an actual historic event, worldwide (global) in its extent and effect.
- » The special creation of Adam (as one man) and Eve (as one woman) and their subsequent fall into sin, is the basis for the necessity of salvation for mankind (and thus for the Gospel of Jesus Christ).
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Please note that in all of this, we openly proclaim that our work is centred around Jesus Christ. We are convinced that the real needs of men and women can only be met by reconciliation to God through faith in and commitment to Jesus Christ the Creator, as Lord and Saviour.

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# Resolving the Archean Belts in the context of Noah's Flood

Carl Froede, Jr, and A. Jerry Akridge

**E**arth's continents are a patchwork of many different types of geologic materials—sedimentary, metamorphic, and igneous. In many places, similar rocks are grouped and defined collectively. The rocks of the Archean are no exception:

“Archean cratons [protocontinents] expose two broad groups of rocks that are distinguished on the basis of their metamorphic grade: *greenstone belts* and *high grade gneiss terrains*. Both groups are intruded by large volumes of granitoids. Together these rocks form the *Archean granite-greenstone belts*.<sup>1</sup>

Secular uniformitarian workers claim that Archean granite-greenstone belts are the oldest exposed rocks on Earth, ranging between 4.0 and 2.5 Ga in age,<sup>2</sup> and are believed to have formed the first continents.<sup>1</sup> Geologically, they are defined as:

“A large area of exposed basement rocks in a craton [continent], commonly with a very gently convex surface, surrounded by sediment-covered platforms. ... The rocks of virtually all shield areas are Precambrian.”<sup>3</sup>

## Possible origins

Two young-Earth creationist interpretations have been offered to explain the many Archean belts exposed on Earth's continents. The first assigns them to the biblical Creation Week<sup>4,5</sup> (Days 1 and 2) while the other defines their formation with the onset of and during the Flood<sup>6-8</sup> (figure 1). Both positions derive their understanding

from the same geologic datasets in defence of their ideas. We briefly review these perspectives.

### Proposal 1. The Archean formed during Creation Week

In their ground-breaking book, Whitcomb and Morris assign the Archean rocks to the first day of Creation Week:

“... many of those rocks now called Archaeozoic ... also known as the ‘basement complex’ apparently underlie all other crustal rocks and are almost entirely composed of igneous and metamorphic rocks.”<sup>9</sup>

Because so little was known of the Archean when their book was published, Whitcomb and Morris offered no further understanding in their interpretation of these rocks.

More recently, young-earth creation geologists Dickens and Snelling defined the continental rocks that compose the Archean belts as having formed during the first two days of Creation Week, based on their superpositional order and extreme radiometric ages assigned by naturalistic geologists.<sup>10</sup> Additionally, they claim that the Archean rocks/strata, by nature of their similar geologic composition and form, unite them globally to a common origin:

“... we aren't surprised that in the observable sequences of mappable rock units there are significant patterns that would seem to relate to God's creative work in designing the earth as man's home. For example, komatiites (high magnesium basalts) and granite-greenstone belts are characteristic of the so-called Archaean at the base of these rock sequences. ... This same pattern is found in comparable rock sequences on other continents.”<sup>11</sup>

Referring to the specific biblical time of Archean Belt formation, Dickens and Snelling state:

“It is concluded that global scale geological work was done in the

Creation Week and not just in the Noahic Flood.”<sup>12</sup>

Regarding the idea of vertical tectonics in association with the formation of the Archean Belts during the Flood, Dickens and Snelling state:

“Oard has suggested vertical tectonics during the Flood, but has never presented a viable model that can explain the correlation of identical thick sequences of basalt lava flows thousands of miles apart on either side of the Atlantic Ocean!”<sup>13</sup>

### Proposal 2. The Archean Belts formed during the Flood

Max Hunter originally proposed the Archean strata as being Flood-formed, based on:

“[The] upward movement of fluids, and complete disintegration of the structure of the Earth's crustal zone”.<sup>14</sup>

He cited these processes to support his claim that:

“... recently revealed features of Precambrian, and equivalent strata should be considered as evidence of their deposition as Flood strata, and that, specifically, many of the features of the Archaean lithostratigraphic association are the expected products of the intense geo-hydrologic activity associated with the first 40 days and nights of the Flood, recorded in Genesis, Chapter 7.”<sup>15</sup>

## Archean Belts as Flood-formed tectonic features

In subsequent years, the secular uniformitarian concept of mantle plume tectonics has developed in association with Large Igneous Provinces (LIPs), which, in many instances, is a separate and distinct tectonic framework from plate tectonics.<sup>16-18</sup> Similarly, mantle plumes and LIPs do not directly correspond to the accelerated tectonic processes invoked in the Catastrophic Plate Tectonics model.<sup>19,20</sup>

Secular uniformitarians invoke mantle plumes to explain many of the Archean greenstone-granite terranes across Earth:

“The 2.7 Ga Eastern Goldfields superterrane of the Yilgarn craton (herein east Yilgarn craton) in

Western Australia is a richly mineral-endowed crustal element that has been a prime focus of debate between proponents of an uniformitarian, plate-tectonic–driven interpretation, and advocates of an alternative model wherein

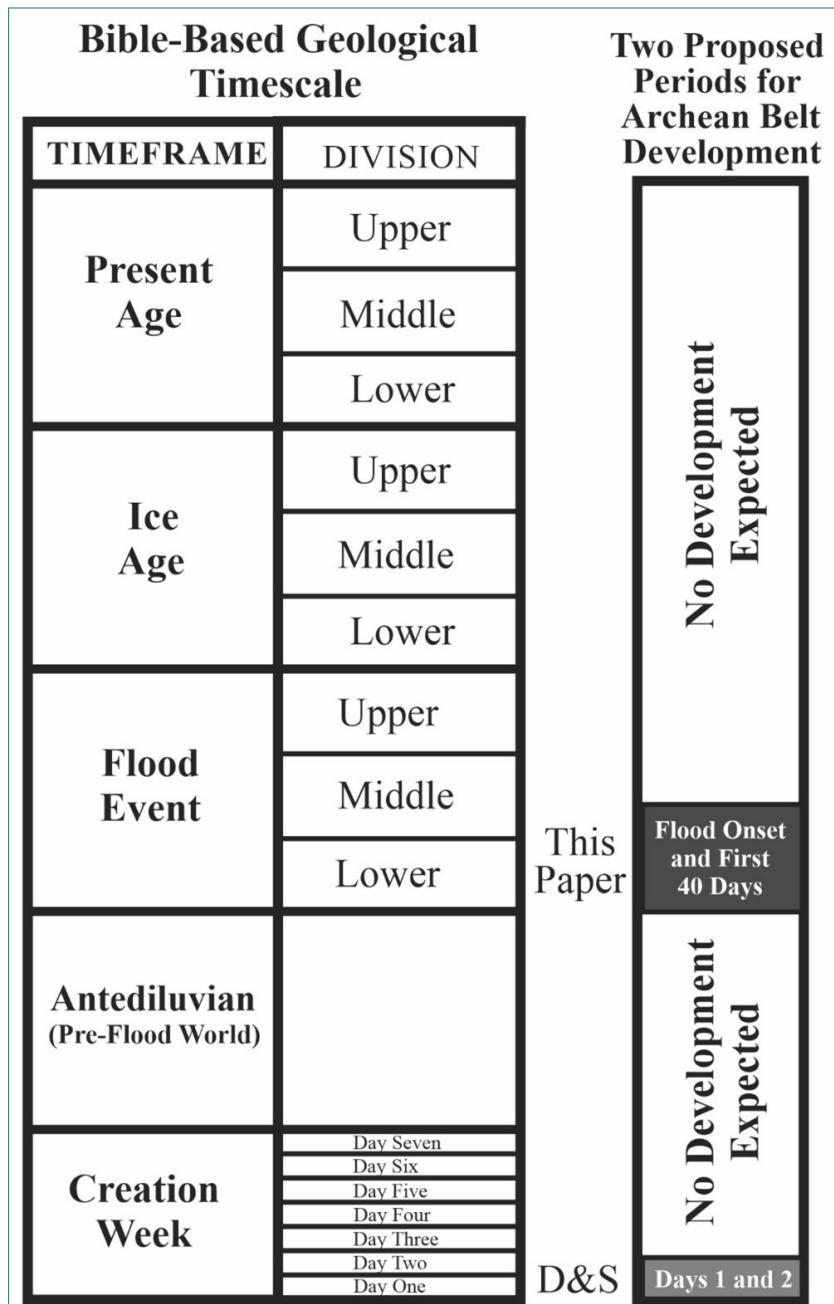
the entire assemblage of igneous rocks is derived ultimately from mantle plume activity.<sup>21</sup> ... Plume–crust interaction [mantle plumes], rather than plume–arc interaction [PT/CPT], provides a much simpler explanation for the tectonic and stratigraphic evolution of the east Yilgarn craton lithosphere, and potentially for other typical Archean greenstone belts.”<sup>22</sup>

“Geochemical analyses of basalts from the Pilbara Supergroup [Western Australia] indicate two distinct compositional groups that are intimately interbedded throughout the succession. ... The composition of the high-Ti basalts, and their source, did not change significantly throughout the 300 m.y. period of eruption of the lower Pilbara Supergroup. These basalts, and associated komatiitic magmas, formed from a succession of mantle plumes.”<sup>23</sup>

“Each plume event [across the Archean Pilbara Craton] resulted in eruption of thick dominantly basaltic volcanic successions on older crust to 3.72 Ga, and melting of crust to generate first tonalite-trondhjemite-granodiorite (TTG), and then progressively more evolved granitic magmas. In each case, plume magmatism was accompanied by uplift and crustal extension.”<sup>24</sup>

Mantle plumes have also been proposed for other Archean Belts with similar structure and rock composition:

“The 2724–2722 Ma Stoughton-Roquemaure Group (SRG) of the Abitibi greenstone belt (the Archean Superior Province, Canada) is a  $\leq 2$  km thick komatiite–basalt succession intermittently exposed for about 50 km along strike. ... The evolution of this Archean mantle plume from inception to demise compares favorably with the Yellowstone hotspot which is assumed to have developed over 17 m.y. and had a diameter of about 300 km.”<sup>25</sup>



**Figure 1.** The two opposing interpretations are presented in a biblical geologic framework. D&S (Dickens and Snelling) propose the Archean Belts formed in the first two days of Creation Week. An alternative (this paper) suggests that many of the Archean Belts began with the onset of the Genesis Flood with some continuing in development through the first 40 days of that catastrophic event.

“The fact that so large a mass of orthogneisses with various compositions and origins were formed in such a short period at the end of the Neoarchean in eastern Hebei Province and other places in the North China craton means that the tectonic setting should be regionally planar rather than linear. The regional thermal background is generally associated with the underplating of basic magmas having resulted from the mantle plume.”<sup>26</sup>

“The arrival of mantle plumes from the deep mantle can be convincingly recognized through large volume–short duration (<10 Ma) magmatic events, so-called LIPs. In the older record, where the flood basalt signature is lost, the identification of giant dyke swarms and the presence of high-Mg rocks (picrites and komatiites) is key. Furthermore, small volume melts, carbonatites, and kimberlites may, in some cases, be indicative of plumes.”<sup>27</sup>

“Assuming that the period 2.75–2.65 Ga corresponds to a single, but global, geodynamic event, we investigate—through numerical experiments—the mechanisms that could have led to the profound continental reworking that occurred at that time. … Our favoured model involves a global rearrangement of convection cells in the deep mantle and formation of multiple mantle plumes. The greenstones emplaced at the surface and the plumes that spread in the thermal boundary layer contributed to heat the crust from both above and below. This produced massive crustal partial melting that reached its climax ca. 40 Myr after the emplacement of the plumes and associated greenstone cover rocks. This led to gravitational instabilities in the crust, as dense greenstone cover rocks began to sink into the thermally softened crust and

granite domes rose in response. The extraction of heat-producing elements toward the upper part of the crust has contributed to the cooling and stabilisation of the cratons.”<sup>28</sup>

If the Flood event timeframe<sup>29</sup> includes incredible geologic activity and tectonic events<sup>30</sup> like mantle plumes, akin to Hunter’s suggestion,<sup>15</sup> then it is not unreasonable to define a number of Archean Belts (based on the evidence) as Flood-formed. Their initiation from the mantle would create areas of crustal uplift that would have been subjected to the highly erosive conditions expected during the Flood. Possible kilometres of uplift would be transformed to the corresponding generation of kilometres of eroded sediments. These sediments likely represent the Precambrian (Paleoproterozoic to Neoproterozoic) materials commonly found in many of the Archean Belts.<sup>31</sup>

We believe that some of the mantle plumes continue into the present as isolated hot spots (e.g. Iceland,<sup>32</sup> Yellowstone, and the Hawaiian Islands),<sup>33</sup> while others are no longer rising or they occur in areas of slow subsidence. However, we make no claim that all Archean granite-greenstone belts are the result of rising mantle plumes. Moreover, as noted above, creationists have put forward different perspectives on the placement of the Archean in biblical history. An evaluation of the relative plausibility of different proposals is beyond the scope of this article. We simply wish to note how recent research advances Hunter’s previous suggestions<sup>15</sup> for contextualizing the Archean within Noah’s Flood. Still, further research and discussion in this area is needed. Nonetheless, mantle plume tectonics provides young-Earth creationists with a means of understanding the origin for some of the Archean Belts and can be adapted to explain conditions associated with the catastrophic Genesis Flood.

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31. The questions raised by Davidson and Hunter regarding the preservation of raindrops in the mid-Mesoprotozoic Venterdorp Supergroup of South Africa are easily accommodated in the mantle plume tectonic model. These areas experienced uplift with the Flood-eroded sediments transported to adjacent basins. Some of the eroded sediments were exposed to rain (forming the raindrop impressions) as the basins were filled. Other materials (e.g. organic carbon sources) in the area undergoing uplift could have been incorporated in the growing sedimentary pile as the Flood progressed. See discussion in (1) Davison, G.E., The importance of unconformity-bounded sequences in Flood stratigraphy, *J. Creation* 9(2):223–243, 1995, and (2) Hunter, ref. 8. We contend that the geologic energy released across the earth, beginning with the Flood, is beyond anything we can presently completely comprehend. In understanding the formation of Archean Belts, it is apparent that the words in 2 Peter 3:6 take on greater meaning and demonstrate the magnitude of changes the earth experienced tectonically and geologically during the Flood.
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## Saturn's changing rings

Wayne Spencer

In 2017 the *Cassini* spacecraft finished its mission at Saturn by making 22 orbital passes between Saturn's D ring and the cloud tops of Saturn itself. This has been called 'Cassini's grand finale'. In the 'grand finale', the *Cassini* spacecraft flew just 1,600 to 4,000 km (1,000–2,500 mi) above Saturn's clouds. After making these passes over Saturn's clouds, it ran out of fuel and fell into Saturn. The *Cassini* mission provided a great deal of information about Saturn, its moons, and its amazing rings. Secular scientists long assumed that Saturn's rings were of the same age as the planet, which they would say was 4.6 Ga. But for years creationists have written about evidence for Saturn's rings being much younger.<sup>1–3</sup> Other facts regarding the Saturn system have also been addressed by creationists as confirmations of a biblical creation view.<sup>4,5</sup>

But how should we understand Saturn's rings? Is the age of the rings the age of the planet? Saturn's rings are very dynamic and complex; they can change over periods of just a few hours in some details. Naturalistic scientists assume our solar system to be 4.6 Ga in age, having formed out of

a spinning disc of gas and dust. But in recent years planetary scientists have acknowledged growing evidence that Saturn's rings are much younger than the alleged old age of Saturn and have thus come to a general consensus that Saturn's rings did not form with Saturn but formed much later.<sup>5</sup>

The *Cassini* mission to Saturn provided more definitive data regarding the mass and density of the rings of Saturn, meteoritic dust falling on the rings, particulate and vapour material falling into Saturn (ring rain), and the composition of the rings. Saturn's main rings are approximately 5 m thick from the inner edge of the C ring going outward to the outer edge of the A ring, which is 30 m thick (figure 1).<sup>6</sup> These thicknesses do not apply to the F, G, and E rings outside the A ring, since they consist of diffuse dust. In the main rings (A, B, and C) the ring objects range mostly from about 1 cm to 10 m in size.<sup>7</sup> The *Cassini* mission refined the mass estimate of Saturn's rings to be 40% of the mass of the moon Mimas.<sup>8</sup> The main rings are the A, B, and C rings, which do not have large amounts of dust. However, the inner D ring and the outer F, G, and E rings have more dust. In composition, the ring objects are estimated to be more than 95% water ice.<sup>8</sup> There are also small concentrations of other substances that fall on the rings, often referred to as 'pollution'.



Image: NASA and STScI

**Figure 1.** Image is in infrared light from the James Webb Space Telescope, taken 25 June 2023 (cropped). Rings appear bright, showing the narrow F ring on the outside and the A, B, and C rings within. The D ring is faint but lies inside the C ring.

### Slightly polluted rings

One study from Zhang *et al.*<sup>7</sup>, in 2017, estimated the amount of non-icy material that impacted on the rings from hypervelocity micrometeoroids for Saturn's A and B rings, and the Cassini Division. This used microwave radiometry from the *Cassini* spacecraft. This method involved measuring the degree of scattering of the microwaves based on reasonable assumptions of the type of particles falling on the rings' icy objects and how they transferred across the rings. This estimates the rate that micrometeoritic material is being added to the icy ring objects. Zhang *et. al.* summarized their results as follows:

"The pollution exposure time in the B ring, Cassini Division and A ring all lie between ~10–150 Myr, which is also consistent with the exposure time due to micrometeoroid bombardment we derived for the inner and outer C ring. These results taken together support the idea that Saturn's rings are geologically young, 150 Myr old, further suggesting a formation scenario in which the rings are derived from the relatively recent breakup of an icy moon, perhaps of Mimas' mass ... ?"<sup>7</sup>

Additional research has been done since 2017 which looks into two other phenomena to estimate the age of Saturn's rings. One aspect is to estimate the effects of meteorites, ions from interplanetary space, and other particles from the moons as they impact ring objects. This leads to what's called ballistic transport. Ballistic transport in Saturn's rings occurs when a small impactor strikes a ring object, and ejecta is scattered from the impact. This ejecta scatters predominately in the prograde direction (the direction of rotation of the rings around Saturn). But it also has other effects. These small impacts cause a small loss of angular momentum that affects the orbit of the ring object impacted. The ring object that is impacted may also lose a small

amount of mass from the impact. Thus, as impact ejecta is scattered across the rings, it tends to cause multiple ring objects to drift inward due to loss of angular momentum. The ejecta may also kick up other particles. This leads to some particles drifting inward and falling into Saturn's upper cloud layers. This becomes an age indicator from a) the erosion of the ring objects by the impacts, and b) the transport of particles and even some vapours inward to Saturn. Impacts on moons that are within or near the rings of Saturn possess a large fraction of their mass as ice, and some of them can possess some organic compounds. Thus, some gases may transport inward to Saturn's clouds as well. These transport processes have been studied by scientists very seriously since the end of the *Cassini* mission. The 'grand finale' also provided direct close-up spectrometry for particles between the inner D ring and Saturn. The *Cassini* spacecraft also sent some data from within the upper layers of Saturn's clouds even as it descended into the planet.

### Influx to Saturn

Durisen and Estrada<sup>8</sup> do an analysis of the impacting particles as well as the ejecta in ballistic transport across Saturn's rings. Instruments used on the *Cassini* spacecraft for this include the Cassini Cosmic Dust Analyzer (CDA) and the Cassini Ion and Neutral Mass Spectrometer (INMS). The Cosmic Dust Analyzer found that the likely source of the impactors affecting the Saturn system was the Trans-Neptunian region. The micrometeoroid particles do not travel at the higher speeds that would make them like long-period comets, and their composition is more like Trans-Neptunian objects as well. This aspect was not what scientists expected. It had been thought they would have their source in the Oort cloud. Durisen and Estrada describe their observations:

"The Cassini Ion Neutral Mass Spectrometer (INMS) experiment, which measured the composition of Saturn's equatorial upper atmosphere and its interactions with

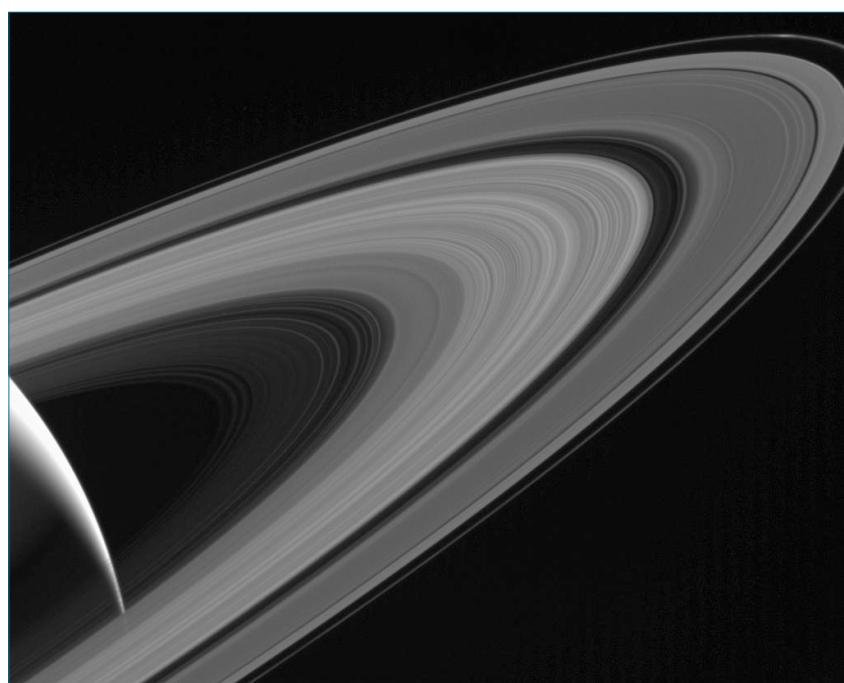


Image NASA/JPL-Caltech/Space Science Institute

**Figure 2.** Picture is taken in visible light, from the *Cassini* orbiter on 13 May 2017, using *Cassini*'s wide-angle camera. The faint strands of the D ring are shown in the dark inner edge of the main rings.

material originating from the rings, found a surprisingly large mass influx of between 4,800 and 45,000 kg/s within a latitude band  $8^\circ$  near the equator . . . In addition to observing the infall of water, substantial amounts of volatiles and impact fragments of organic nanoparticles were also measured.”<sup>8</sup>

The above study made estimates regarding the average number of ejecta particles generated per impactor, the numbers of particles that can jump from one region to another in the rings, and other factors. There are a number of uncertainties in these estimates, but the data from *Cassini* does provide a basis for such calculations. The D ring (figures 1 and 2) lies inside the C ring and is the ring closest to Saturn’s clouds. Thus, C and D would be expected to be the rings with the lowest ‘lifetimes’. It is thought that the C ring provides some replenishment of the D ring. In fact, it is suggested that the D ring could disappear and reappear on short time frames such as a year or a few years, due to events occurring in the rings. Durisen and Estrada summarize the results of their analysis:

“From our own estimates of the mass inflow rates due to BT [ballistic transport] alone . . . we can calculate the remaining ring lifetime. Taking the current ring mass to be 0.4 Mimas masses . . . or  $\sim 1.5 \times 10^{19}$  kg, we find that the range of times for the remaining mass of the rings to fall into the planet is . . .  $\sim 150$  to 400 Myrs.”<sup>8</sup>

Thus, the new data from the *Cassini* mission points to the conclusion that significant material is being added to Saturn’s atmosphere. This phenomenon is generally referred to as ‘ring rain’. Another qualitative confirmation of this comes from a study of the composition of the particles and gases present in Saturn’s atmosphere. The ‘grand finale’ for *Cassini* included five months during which the spacecraft passed between the D ring and Saturn. This meant that *Cassini* actually passed through the

top layers of Saturn’s atmosphere in its last five orbits. Scientists expected that the only gases from Saturn that would be encountered would be H<sub>2</sub>, atomic hydrogen, and helium. It was assumed that other heavier gases from Saturn would be present only in deeper layers. However, the INMS instrument detected other molecules, including methane, water, ammonia, carbon monoxide, carbon dioxide, and molecular nitrogen (N<sub>2</sub>), along with other hydrocarbons, and dust.<sup>9</sup> These gas and vapour molecules would significantly affect the observed composition of Saturn’s upper atmosphere over billions of years. But this effect on the composition is not observed, even though the influx of these materials is very significant. Therefore, this is another confirmation of the rings being young.

### Implications and conclusions

Due to the definitive data from *Cassini*, there is no longer an option for naturalistic scientists assuming an old age for the solar system to say Saturn’s rings formed with the planet. They have accepted that Saturn’s rings must be much younger than the planet. One research team separate from Durisen, above,<sup>10</sup> said the following:

“We find that the ring exposure age for the current mass influx into the Saturnian system does not allow the rings to be formed together with Saturn and its satellites . . . nor slightly later during the Late Heavy Bombardment . . . Saturn’s current rings cannot be primordial.”<sup>10</sup>

Therefore, scientists are now forced to investigate various catastrophic breakup or collision scenarios to explain the formation of the rings. It is also common for scientists to suggest that Saturn’s rings were at one time more massive than they are today.

To young-age creationists, however, it is still a valid option to think of Saturn’s rings as created with Saturn in the Creation Week only several thousand years ago. This still agrees with the latest data from *Cassini*. On

the other hand, a biblical creation perspective may not require making the assumption that the rings were created with the planet. The ring age determinations above are rough upper limits, so the true age of the rings could be younger. Creationists should not understand Saturn’s rings as if every feature we see was created in the Creation Week as we see them today. The *Cassini* data may suggest some event or events in the past since creation that caused micrometeoroid impacts in the outer solar system. There are a number of ongoing phenomena in Saturn’s rings that are explicable by well understood physics and which do not require millions or billions of years. There is a need for more research from creationists to clarify what processes can feasibly take place in timeframes on the order of 6,000 years.

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# A new ‘marine crocodile’ discovery on the Jurassic coast of England

Andrew Sibley

Fossil hunters working on the Jurassic coast of England discovered a new thalattosuchian fossil in 2017 (‘suchus’ is the Latinized form of the Greek ‘soukhos’; meaning crocodile). This extends the evolutionary narrative of this creature possibly back to the Late Triassic (Rhaetian) from the Early Jurassic. The account has recently been published in the *Journal of Vertebrate Paleontology*.<sup>1</sup>

Thalattosuchian fossils are sometimes referred to as extinct marine crocodiles, although they are not strictly classed with the Crocodylia. Instead, they are referred to as a clade of marine crocodylomorphs, although the phylogenetic narrative is equivocal. They are considered to be either members of Neosuchia (which includes modern crocodiles and other closely related fossil crocodylomorphs) or older members of Crocodylomorpha.<sup>2</sup> Although the clade had a wide oceanic distribution, specimens have also been identified in freshwater settings.<sup>3</sup>

According to evolutionary theory, thalattosuchians and crocodylians are claimed to have transitioned from quadrupedal terrestrial animals (i.e. from sphenosuchians) in the Triassic. Dating has previously restricted the earliest extinct animals to the Early Jurassic / Early Cretaceous.

Two subgroupings have been ascribed to the clade: the Teleosauroidae and Metriorhynchoidea. Teleosauroids are similar to other crocodyliformes; they were not highly adapted

to life in the ocean, and they possessed typical crocodile features such as tail osteoderms. The Metriorhynchidae are said to have been more highly adapted to survival in an oceanic environment—limbs were transformed into flippers, with smoother scaleless skin and the possession of a tail fluke.

## New discovery

The new discovery, from the Charmouth Mudstone Formation, includes part of the head, backbone and limbs, and is sufficiently complete for it to be identified and named. It is said to be the only thalattosuchian from the early Jurassic Pliensbachian age (185 Ma).<sup>4</sup> The name *Turnersuchus hingleya* (figure 1) has been given after Paul Turner, who found the first fossils and donated the specimens to the Lyme Regis Museum (Dorset, England), and Lizzie Hingley, who prepared the find. Associates from the nearby Charmouth Heritage Coast Centre helped to piece the various fossils together.

Following this finding, it is now suggested that the Thalattosuchia evolved earlier, in the Late Triassic, although with limited supporting evidence—the notion that they

lived prior to the Jurassic is based on time-calibrated phylogenetic analysis, which partly constrains dating by stratigraphy.<sup>1</sup> Separately, a thalattosuchian skull has been discovered in a cave system in Morocco from rock layers dated to an age prior to the Pliensbachian.<sup>5</sup> Evolutionary scientists therefore suggest that these latest finds are basal to both Teleosauroidae and Metriorhynchoidea. It is suggested that *Turnersuchus* is basal because it possesses fewer derived character states than the other known thalattosuchians. Thus, the evidence for it being basal is partly its morphology, but filtered through phylogenetic analysis.<sup>1</sup> The lack of further fossil evidence from the Late Triassic would imply, from an evolutionary perspective, that there is a ‘ghost lineage’ of yet-to-be-discovered fossils.

The closest modern crocodilian form is the gharial (family Gavialidae) (figure 2), which has a long, slender snout for catching and eating fish, and today lives in rivers of the Indian subcontinent. Although some similarities are evident, the researchers have claimed the shape of the *Turnersuchus* skull is notably different from the



Image: Júlia d' Oliveira

**Figure 1.** Artistic impression of *Turnersuchus hingleya*, claimed to be one of the oldest marine crocodylomorphs ever found (from ref. 4).

modern form, and that it is only distantly related to modern crocodiles.

The shape of the supratemporal fenestrae in the skull suggests it had a powerful and fast-biting action to help catch its prey of fish and cephalopods. Like modern crocodiles, this may have helped with the temperature regulation of the animal's brain. The further speculation is that the 2-metre-long *Turnersuchus* found in the Charmouth Mudstone Formation gave birth to live young, and so was not an egg layer as are modern crocodiles, although this is a claim that is unsupported by evidence.<sup>4</sup>

There is further evidence that the animals were already perfectly adapted to life in their environment. High resolution studies of the inner ear vestibular system of 18 pelagic thalattosuchian skulls (i.e. the metriorhynchoids, but not *Turnersuchus*), using computed tomography (CT), reveal a compact thickened, and reduced bony labyrinth, which closely resembles that of other marine reptiles, and even whales.<sup>6–8</sup> These animals, that lived in the open ocean, were already well suited to their environment. The semi-aquatic teleosauroids had labyrinths similar to modern crocodylians.

## Discussion and summary

This is an interesting find of another vertebrate fossil along the Jurassic Coast. This coast is famous for finds by Mary Anning, and other 19<sup>th</sup>-century geologists, of plesiosaur and ichthyosaur fossils. Among land-living vertebrate fossils identified from these rock layers is *Scelidosaurus*,<sup>9</sup> which has been found in the same layers as *Turnersuchus*. With *Scelidosaurus*, skin impressions and stomach contents have also been found, which points to rapid burial in these layers. With evidence of rapid burial in the Charmouth Mudstone Formation from these other finds, as even admitted by secular research, we call into question the dating estimates. How can rock layers be dated accurately by the extension of physical sedimentary processes, when rates of sedimentation are believed to have varied significantly?

Although there may be differences between *Turnersuchus* and the gharial crocodile, these differences are often exaggerated by the evolutionary narrative. Like many finds in the fossil record, we see that there is evidence of sudden appearance, and subsequently only relatively small changes in

morphology. Many of the unique character states of thalattosuchians are present in *Turnersuchus* (which is believed by evolutionists to be an early stage in the evolution of the group), so evolutionists are still faced with the problem of explaining the origin of thalattosuchians. The thalattosuchian specimens appear suddenly in the fossil record with an assumed reconstruction now back to the Late Triassic. And yet they were already well suited to their environment. This is consistent with intelligent design, and belief that the fossil record indicates rapid burial during the Noahic Flood.

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**Figure 2.** *Gavialis gangeticus* is believed to be the closest modern crocodilian to *Turnersuchus hingleyae*.

# Circular reasoning used to date old fossils in old rocks ‘Down Under’

Andrew J. Fabich

**E**volution of eukaryotes from a common ancestor with prokaryotes is a significant development on the evolutionary timescale. According to evolutionary theory, this historic event must have occurred after the origin of the first cell. While evolutionists have inappropriately cited evidence of biochemical signatures in rocks for the origin of prokaryotic life on Earth, they only recently uncovered evidence comparable to these biochemical signatures for eukaryotic life. Living things today leave marks in rocks like these, so why are these eukaryotic biochemical signatures any different? The authors inappropriately conclude that these biochemical signatures are signs of old life because they found them in rocks assumed to be old. From

a biblical worldview, we understand that the biochemical signatures in the rocks indicate a global Flood.

## Lost world of former ecosystem

According to evolution, the first cell came into existence in a relatively short amount of time after the earth came into existence, approximately 4.5 billion years ago. The evidence cited by evolutionists is based on impressions of what look like bacteria in rocks known as ‘stromatolites’. The next major event on the evolutionary timeline is when the ancient archaeon cell engulfed a bacterium to form the first eukaryotic cell in what has been called the ‘Endosymbiotic Theory’. In an attempt to demonstrate this, evolutionists have gone hunting for microfossils of eukaryotic cells. Until recently, the only presumably eukaryotic microfossils they could find were present in rocks dated 1,050 million years ago.

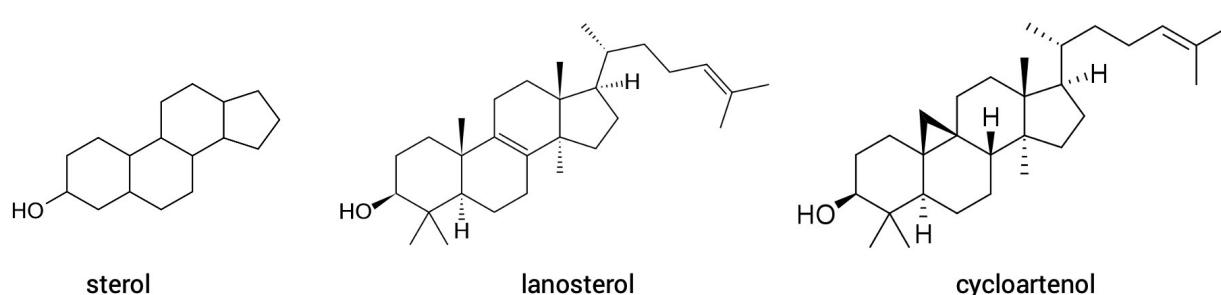
The authors of the study state that they

“... report the discovery of abundant protosteroids in sedimentary rocks of mid-Proterozoic age. These primordial compounds had previously remained unnoticed because their structures represent early intermediates of the modern

sterol biosynthetic pathway ... . The protosteroids reveal an ecologically prominent ‘protosterol biota’ that was widespread and abundant in aquatic environments from at least 1,640 to around 800 million years ago and that probably comprised ancient protosterol-producing bacteria and deep-branching stem-group eukaryotes.”<sup>1</sup>

The ‘protosterols/protosteroids’ found are what is claimed to be the discovery, for the first time, of indications of eukaryotic life. A protosterol is a chemical found in eukaryotic cells that resembles the class of compounds we know as sterols/stereoids (figure 1). The authors claim that this particular kind of sterol is a primitive form of a sterol that left a signature behind in these old rocks. The previous evidence for ancient eukaryotic life was what is referred to as ‘crown eukaryotes’. The crown eukaryotes are called this because they appear in the Darwinian tree of life after the emergence of the eukaryotes and not at the base of when eukaryotes supposedly evolved first. The name given for eukaryotes near the base of the branching point on the evolutionary tree is ‘stem eukaryotes’. The protosterols identified align with their interpretation of what are called ‘stem eukaryotes’. Therefore, these authors conclude that

## Comparison of protosterols with sterol



**Figure 1.** Shown at left is the core backbone of a sterol. At middle and right are lanosterol and cycloartenol, which are protosterols and represent the precursor to molecules like cholesterol and the steroid hormones. The conclusion that these compounds in rocks indicate eukaryotic life is likely correct. But evolutionists who do not assume the Bible's truth about the fossil record (i.e. the Flood of Noah's day) incorrectly interpret *when* that life existed.

Sterol: Roland Mattern; Wikimedia/PD; Lanosterol: Fvasconcelos, Wikimedia/PD; Cycloartenol: Mykhailo Wikimediia/CC0

the rise of eukaryotic life occurred much earlier than previously thought and that the crown of eukaryotic life was well established in the fossil record from the previous evidence.

### Shaky foundations on evolutionary (proto)sterols

Perhaps the most significant problem with this style of thinking is that it is circular reasoning to assume protosterols are old because they are found in old rocks. The idea that bacteria are capable of corroding metals like iron is over a hundred years old.<sup>2</sup> It is well established that the bacteria growing and thriving under conditions where these macro- and microfossils are isolated begs the question as to whether the microfossils were formed recently or in the distant past: both positions require faith to answer the question.

The authors of the study very clearly demonstrate that they detected these protosterols. There is no reason to question whether these protosterols were made from a living cell because we only know them to come from living cells. However, the authors of this study put the proverbial cart before the horse in assuming protosterols can be dated by looking for their presence in old rock layers (i.e. guilt by association). The protosterols were first synthesized in a lab before chemically testing rocks with presumed old ages. When the authors looked for these protosterols, they found them throughout the entire geologic column, extending into sedimentary rocks of mid-Proterozoic Age (isolated from the Barney Creek Formation, Northern Territory, Australia). Finding protosterols in deep rock layers is significant because no eukaryotic index fossils exist in this part of the geologic column. Ultimately, not finding old fossils in old layers is a form of circular reasoning because they assumed ancient ages for these

compounds and then found them in rocks already claimed to be old, rather than dating these molecules using different methods. While the use of index fossils has its place under very specific circumstances, the authors of this paper are essentially trying to establish a new set of index fossils, and this warrants paying some attention to.

### Deep protosterols discovery supports the biblical model

Based on God's Word, we know that everything was created roughly 6,000 years ago, and that there was a catastrophic Flood in the days of Noah (Gen. 6–9). Everything on the planet at the time of Noah's Flood was preserved in the geologic column and represents former ecosystems instead of deep time. If we look at the finding of protosterols present in the geologic column through the lens of Scripture, we must realize that it is telling us something about a particular ecosystem. It is noteworthy that the authors of this study unknowingly state as much in the abstract of their paper (and throughout for that matter):

"Modern eukaryotes started to appear in the Tonian period (1,000 to 720 million years ago), fuelled by the proliferation of red algae (rhodophytes) by around 800 million years ago. This 'Tonian transformation' emerges as one of the most profound ecological turning points in the Earth's history."<sup>1</sup>

Instead of paying attention to the supposed profound change of an ecosystem millions of years ago, we can stand confidently on God's Word, knowing that "the world that then existed was deluged with water and perished" (2 Peter 3:6): including ecosystems! It is striking that the description for these protosterol fossils uses ecological terms (i.e. language that points to a global Flood).

In particular, the finding of protosterols is expected from a biblical hypothesis instead of an evolutionary hypothesis, because we know that creation of the biosphere was complete by Day 6 of Creation Week (Genesis 1:31). So biblical creationists expect to find traces of former life throughout the fossil record, including layers yet uninvestigated. The idea of finding protosterols everywhere was also mentioned by BigThink, stating, "the protosteroids were ubiquitous, showing up in rock samples from ecosystems around the world." Having ubiquitous protosterols in the fossil record is something that fits with a global Flood in Noah's day. In fact, I have previously pointed this out in highlighting that modern-day microbial biogeography (i.e. where bacteria are found all over Earth) provides living evidence of a global Flood.<sup>4</sup>

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# Could humans take down mammoths with spears?

Michael J. Oard

Uniformitarian scientists are still battling over what caused about 67% of mammals over 45 kg to go extinct after their ‘last ice age’.<sup>1,2</sup> In some cases, extinction occurred on one continent but not on others. The percentage of extinctions varies on each continent (table 1) and includes mammoths, mastodons, saber-toothed cats, huge ground sloths, glyptodonts, toxodonts, and diprotodonts. Examples of mammals extirpated from North America, but not elsewhere, include the horse and camel.

## Overkill or overkill?

Hardly any extinctions occurred after the other 50 or so presumed previous ice ages of various intensities in the uniformitarian model.<sup>3</sup> This strongly suggests two possibilities: (1) their previous ice ages never happened, or (2) some unique event occurred only at the end of the last ice age. Since

uniformitarian scientists universally believe the second option, they have developed competing theories.<sup>4</sup> Some think the unique change is the migration of humans all over the earth, especially to the Americas and Australia. These scientists believe in the ‘overkill’ model of extinction, claiming humans caused the extinctions. The ‘overkill’ model, an offshoot of overkill, proposes that the diseases and rats that accompanied human migration caused most of the extinctions. Few scientists believe this today. The other main theory is ‘overkill’ in which climate change killed them off. Both the overkill and overkill theories can explain some of the data but fail to explain all of it.

## Mammoth hunters?

Mammoths lived over much of the mid and high latitudes in the northern hemisphere. Spear points have been found associated with the bones of mammoths and other large mammals in the United States at about a dozen locations.<sup>5</sup> So, it has been assumed that the Clovis people, once believed to be the ‘First Americans’, quickly killed the mammoths with spears having unique stone points. However, this view is coming under challenge: “But the Clovis people’s status as adept killers of tusked beasts weighing up to about 9 metric tons has come under fire.”<sup>6</sup>

## Some say the spear points could not penetrate a mammoth

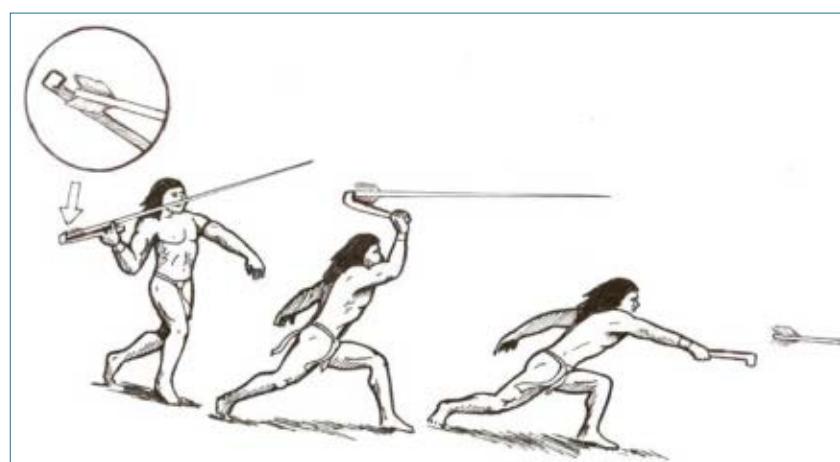
The main problem comes from research showing that, during direct hunting, the Clovis points would rarely be able to penetrate the hair, hide, or fat of a mammoth, even with a spear thrower, called an ‘atlatl’ (figure 1):

“It’s not clear that Clovis points attached to spears could even have penetrated a mammoth’s hide,’ Eren says. ‘We need to stop assuming that Clovis people and earlier Stone Age groups (in Asia and Europe) must have been mammoth hunters [brackets in original].’”<sup>6</sup>

Metin Eren had earlier stated, in 2015, that the Clovis spears could easily take down a mammoth, but he changed his mind after conducting research on mammoth characteristics and the momentum of a Clovis spear.<sup>7</sup> Based on frozen carcasses in Siberia and the skeletons of mammoths in museums, Eren *et al.* discovered that the internal anatomy was protected very well. Frozen carcasses in Siberia showed that woolly mammoth skin was 2–3 cm thick on average, and below the skin lay 8–9 cm of fat. The hide was covered by 5–15 cm of dense underfur topped by outer layers of hair 10–60 cm long. A Clovis point had to penetrate 17–30 cm into a woolly mammoth and avoid a picket fence of ribs. In a lab setup with different Clovis points, Eren *et al.* simulated a

**Table 1.** Percentage of mammalian megafauna over 44 kg (100 lb) that went extinct during and around the Late Pleistocene on all continents except Antarctica.<sup>1,2</sup> Southern Eurasia is not included because of insufficient data.

Continent	Percent extinct
Africa	25%
Australia	88%
Northern Eurasia	36%
Northern America	72%
South America	83%



**Figure 1.** An atlatl (spear thrower) in use



**Figure 2.** Clovis points from the Rummells-Maske Cache Site, Iowa

spear hitting a target and concluded that Clovis points on a spear could only rarely penetrate deep enough to kill the mammoth. The problem is exacerbated by a moving target.

Eren *et al.* also showed that Clovis pointed spears would not have had enough power to kill a large mammal. Also, the Clovis points that should have hit ribs or other bones would have left behind many broken Clovis points at kill sites. They also suggested that the Clovis points could instead have been used to butcher a dead mammoth. Thus, Eren *et al.* believe that it was climate change that caused the demise of the woolly mammoth and other mammals at the end of the ‘last ice age’, although mammoths hung on for a while in the Holocene.

Eren *et al.* also have a well-known ally in archeologist Vance Haynes. He accepts that the Clovis point/mammoth associations could be the result of scavenging and adds that there is no clear evidence of hunting with Clovis points.<sup>8</sup> He further adds that of the 10,000 Clovis points found so far, none have been found embedded in the bones of big game, including mammoths and mastodons. Moreover, the number of associations between spear points and large mammals is very small.

### Some disagree

But other scientists disagree with Eren *et al.*, probably because they are biased toward the overkill point

of view. These critics still believe that Clovis and other people groups in northern Asia killed off the mammoths within a few hundred years.<sup>8</sup> They point out that Clovis points (figure 2) were clearly intended for hunting.<sup>8</sup> They have also countered Eren *et al.* by postulating that Clovis hunters could have wounded the mammoths or mastodons avoiding the rib area, in which case they could follow the wounded animal until it bled to death. In that way, not as many spear points would be damaged. Furthermore, it is not clear how significant the spear point data is to the question of how the Clovis people would’ve hunted mammoths. As Agam and Bankai note, there were other ways to kill a mammoth plausibly available to the Clovis people besides direct hunting. For instance, running mammoths into bogs, pits, or off cliffs, such as observed with African people groups.<sup>9</sup> Therefore, it looks like the debate will continue.

### How would the climate have caused the extinctions?

Eren *et al.* have come to accept that climate change killed off all the beasts. Based on a computer simulation, Fordham *et al.* claim that rising temperatures were the key variable for mammal extinctions:

“Computer simulations based on ancient DNA, fossil and climate data suggest that rising temperatures and growing human populations led to

mammoth die-offs in Europe and Asia starting around 19,000 years ago and in much of Asia [?—sic] starting roughly 15,000 years ago.”<sup>10</sup>

It is questionable that human populations would have grown large enough in a few hundred years after colonization of a new territory to diminish the mammoth habitat, especially in Siberia and Alaska. But the researchers emphasize that *rising temperatures* and wetter conditions shrank the grasslands on which the animals lived at the end of the evolutionists’ very cold ice age.<sup>8</sup> How could a warmer, wetter climate cause such an end-Pleistocene mass extinction? One would think that rising temperatures and melting ice would open up more habitat for the mammals. The question of how they died remains unanswered.

### Biblical Ice Age solution

I believe their confusion is caused by their belief in uniformitarianism, deep time, and evolution. According to the biblical Ice Age,<sup>4</sup> which predominantly corresponds to the last uniformitarian Pleistocene ice age, the early-to-mid-Ice Age climate had mild winters, cooler summers, and much greater precipitation than today. In this environment, trees and grass would flourish in various areas of the earth. It was an ideal environment for the population of mammals leaving the Ark to mushroom in population and spread all over the earth.

But the Ice Age climate was dynamic, and by the end of the Ice Age, winter temperatures were even colder than today, the summers were warming, and precipitation was low. The large animals did not have time to adapt to the rapidly changing climate. This greatly stressed them, and they died from various combinations of climate variables, different on each continent. Human hunting or resource-space competition toward the end of the Ice Age could also have been an additional pressure on the stressed animals. Small animals survived better because they

did not need as much food and were able to multiply faster than large animals. And as I listed earlier as the first explanation for the absence of mass extinctions after previous ice ages, this was because there were no previous ice ages.

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# The non-evolution of the human liver

*Lucien Tuinstra*

**T**he liver is a multifunction accessory organ to digestion, which means that it is not part of the alimentary canal, but external to it.<sup>1</sup> Among other things, it is essential to the healthy functioning of the gastrointestinal and endocrine systems. Introducing digestive juices into the system, liver functions are part of the process of detoxifying and breaking down food components into a form suitable for absorption. Examples of absorbed nutrients are amino acids, mineral salts, fat, and vitamins. These are building blocks for new cells, hormones, and enzymes, as well as an energy source for other processes.

## A selection of functions

The liver has many roles important for the organism's survival: "Liver functions are pivotal to homeostasis and involve interactions with most of the body's organ systems."<sup>1</sup> For brevity, a few of them are described here.

### Carbohydrate metabolism

The liver controls the glucose level in blood by converting glucose into glycogen (glycogenesis) if the glucose level is too high, and vice versa when it is too low. When a person has low blood sugar, the liver can release glucose through the conversion of certain amino acids and lactate, as well as other sugars like fructose and galactose. If the sugar level is too high, the liver can turn glucose into fats, too.

### Protein metabolism

The compound adenosine triphosphate (ATP) delivers energy for most of life's metabolic processes; for example, the manufacture of protein

machines. ATP synthase is one such machine, a motor consisting of 29 proteins, which in turn produces ATP.<sup>2</sup>

Besides accounting for almost a fifth of total body protein synthesis (including ATP synthase),<sup>3</sup> the liver can digest proteins and convert the resultant amino acids into fat, which it is able to store for later use. The initial step in this breakdown process is the deamination of the amino acid, by removing the amino moiety ( $\text{NH}_2$ ), with by-products co-opted into ATP production. At a pH of 7, and even more so in an acidic environment, the alkaline  $\text{NH}_2$  is quickly protonated ( $\text{H}^+$ ) into the toxin ammonia ( $\text{NH}_3$ ),<sup>4</sup> which the liver converts to the much less toxic urea, disposed of in urine.

### Removal of drugs and hormones

A very important function of the liver is the detoxification of drugs such as penicillin, sulfonamides ( $\text{R}-\text{S}(=\text{O})_2-\text{NR}_2$ , with 'R' a chemical group, the simplest being hydrogen), and ethanol (alcohol). It can also chemically change thyroid and steroid hormones, such as estrogens and aldosterone.

### Excretion of bile

The hepatic cells of the liver daily produce nearly 0.5 litre of bile;<sup>5</sup> a basic liquid (pH 7.6–8.6) that has a yellow, brown, or olive-green colour. Bile is needed for fat digestion during and after meals, so is stored in concentrated form in the gallbladder. This secretes about 500 ml of bile per day, a rate that is regulated by the hormone cholecystokinin (CCK), which causes the gallbladder to contract. Bile is mainly water with bile acids and other salts, cholesterol, bile pigments, ions, as well as other materials. The bile salts help the cholesterol to dissolve in the small intestine. Through their emulsifying action on fats, they also break down large fat globules into smaller droplets, as well as preventing

the latter coalescing into larger ones. This increases the lipid surface area for hydrolysis by the pancreatic enzyme lipase. Hepatic lipase controls fat levels in the blood. The bile pigment bilirubin derives from the breaking down of red blood cells (RBCs), as does iron (figure 1). In the intestine, bilirubin gets further broken down into urobilinogen, giving faeces their characteristic brown colour. In diseases where bilirubin removal from the liver is restricted, it collects in other body tissues, giving the skin and eyes a yellow colour (jaundice).

#### Storage

Not only is the liver a storage place for the aforementioned glycogen and fat, it also stores iron and copper, and it

contains reservoirs of vitamins A, B12, D, E, and K. Together with the skin and kidneys, the liver activates vitamin D.

#### Production of heat

With all these activities, it is not surprising that the liver uses a significant amount of energy. With its high metabolic rate, the liver is the main heat-producing organ of the body.

### Evolution of the liver

According to Johns Hopkins Medicine, “More than 500 vital functions have been identified with the liver.”<sup>6</sup>

It beggars belief how all this could have come about in a gradual, goal-less, evolutionary progression. From no liver to a fully developed,

integrated, multi-tasking organ, numerous tasks would need to be put in place, all interdependent with other organs/systems. This would require the successful implementation of a fantastic number of incremental mutational changes.

Unlike other human visceral organs, the liver can fully regenerate after partial tissue loss:

“Liver regeneration involves a complex network where diverse signaling pathways from different cell types regulate the precise control of genes encoding transcription factors needed to recover the hepatic mass.”<sup>7</sup>

If regeneration from a reduced liver is complex, how did this organ arise in the first place?

Phylogeny studies of vertebrate livers are scanty.<sup>8</sup> A popular textbook for vertebrate comparative anatomy, commenting on the liver in a range of organisms, says that its shape “conforms to the space available in the coelom”.<sup>9</sup> This is akin to saying a round peg fits in a round hole. It does nothing to explain either the arrival of the peg, or the hole.

Liver evolution putatively commenced in an ancestral organism probably similar to the lancelet *Amphioxus*, part of the Cephalochordata subphylum and, according to evolutionary thinking, the closest thing to a vertebrate. “The recent discovery of vertebrate liver-specific proteins in the Amphioxus diverticulum supports this hypothesis.”<sup>10</sup> What, then, might be ancestral to the diverticulum? The reason that “this question is traditionally omitted is that the putatively preceding forms (living animals or fossils) apparently do not provide any relevant evidence for the answer”.<sup>10</sup>

### Pinnacle of liver evolution?

The healthy human liver does a mighty job, and, by all accounts, it is

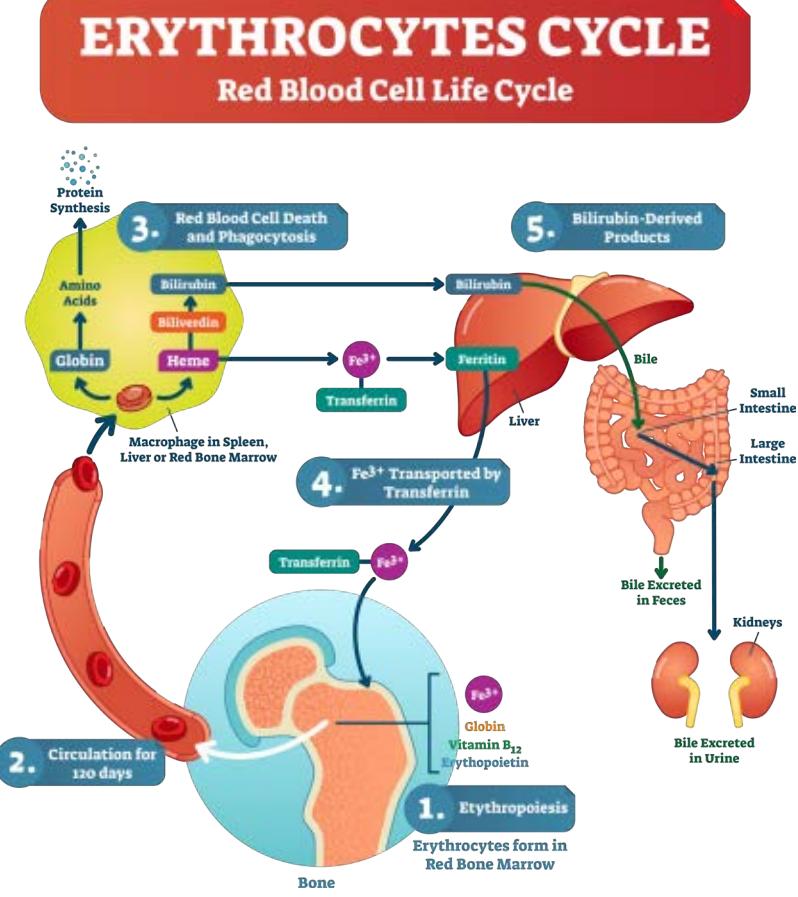


Image: VectorMine, Dreamstime.com

**Figure 1.** Formation and destruction of red blood cells

at peak performance. But assuming evolution brought us to this point, why stop at this apparent summit? Do mutations cease when an organ is functioning well? Unfortunately, mutations are part of life in a cursed creation. A “mutation of a key enzyme involved with the breaking down of glycogen into glucose in the liver … would spell death or a serious problem for the individual”.<sup>11</sup> Mutations are more often than not deleterious,<sup>12</sup> and they have very rarely, if ever, been shown to add any significant genetic information.<sup>13</sup>

Examples of Mendelian liver diseases, caused by hereditary mutations, include haemochromatosis (too much iron), alpha-1 antitrypsin (AAT) deficiency, and Wilson disease (copper accumulation). In such cases, patients’ livers are weakened, or have nearly stopped working altogether. How are these facts of any support for evolution? If a mutation occurred in an animal with a ‘primitive’ liver, how could that improve the liver’s functioning, especially considering the complexity and integrated nature of liver function in the context of other body systems? A conceivable improvement might be a more rapid digestion of incoming nutrients than what is currently achieved, but such enhancement would not be without trade-offs. Another improvement might be achieving the same with fewer resources (e.g. blood-flow).

### Irreducible complexity

Besides glucose concentration, the liver also manages the level of vital nutrients in the blood, such as other carbohydrates and proteins. The way the liver keeps the latter in check is quite ingenious and irreducibly complex, using gated transport. The three main players are a gate in the cell membrane, a chemical sensor, and proteins labelled with an identification tag. When a protein approaches a gate, the sensor checks the ID tag to

determine if the protein may pass, and if so, the gate is opened. If any of these three parts (gate, sensor, tag) is missing, the system fails, and proteins cannot be transported to the right location. If there is no gate, the protein cannot enter or leave the cell, because it cannot go through the cell membrane. If there is no sensor, then the tag cannot be read, and the gate will not be instructed to open. If the protein does not have an ID tag, it cannot be determined whether the protein should be allowed to enter or leave. All three (gate, sensor, tag) would have to evolve and be in place at the same time, or the system would not work, and the creature dies.<sup>11</sup> “The liver’s diverse functions and interactions with other organs accentuate the point that homeostasis requires the *coordinated action of several body systems* [emphasis added].”<sup>1</sup>

### Conclusions

The liver plays a crucial role in the human body. Not only is it included in the digestive system, but it also has important functions that affect other systems. This implies that a gradual evolution of the liver is out of the question. Either the interaction with the rest of the body parts was in place from the beginning, or it would not have come into existence at all, since this interdependency is irreducibly complex.

The evidence fits the creationist worldview much better, as deterioration in livers is apparent, but improvements on healthy ones is not.

The liver is essential for life. Without a liver, death ensues very quickly (Proverbs 7:23).

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# Petroleum systems do not require millions of years

Harry Dickens

A petroleum system is characterized by a genetic relationship connecting a source rock to all the oil and gas it has generated (figure 1). It consists of all the geologic elements and processes that are essential for the formation of a petroleum accumulation.<sup>1</sup> The geologic elements needed are source rock, reservoir, seal, and overburden. The geologic processes involved are trap formation and generation, migration, accumulation, and preservation or degradation of the petroleum.<sup>2</sup> All the elements must be ordered in time and space so that a petroleum accumulation can occur.<sup>1</sup> There is an abundant number and variety of petroleum systems and petroleum fields around the world due to the range of geologic elements and processes in time and space.

The source material for petroleum accumulations is kerogen.<sup>3</sup> Kerogen is a fossilized mixture of dispersed insoluble organic material found in sedimentary rock that, when heated, breaks down into bitumen, oil, and natural gas. There are four principal types of kerogen, which are defined using atomic hydrogen/carbon (H/C) versus oxygen/carbon (O/C), as per the van Krevelen diagram (figure 2). Typical constituents of kerogen are algae and woody plant material.

## Petroleum formation

It is commonly assumed that it takes millions of years for petroleum to form in a sedimentary basin. However, millions of years are not necessary for

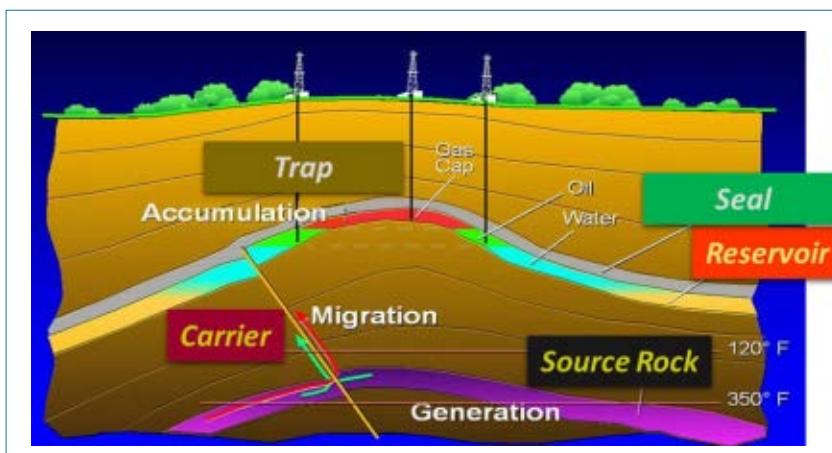
petroleum formation and petroleum can form rapidly. Real-time investigations in natural settings and laboratories show that petroleum can be generated in a period of even a few years or less at appropriately high temperatures and in the presence of water<sup>4</sup> (figure 3). Crude oil has even been made in a laboratory in minutes from algae.<sup>5</sup> Temperature, rather than time, is the most important factor controlling petroleum generation.<sup>4</sup> Temperature increases with increasing burial and with the influence of hydrodynamic water flows.<sup>6</sup> Although, in some areas, such as Australia's Gippsland Basin,<sup>7</sup> petroleum is still forming today, most of the great quantities of oil in reservoirs today likely formed from the burial of organic matter during Noah's Flood and during its aftermath. Petroleum is unlikely to be forming today faster than it is being pumped from the ground.

## Petroleum migration

Primary migration refers to the process of expulsion of hydrocarbons from the source rock. Laboratory hydrous pyrolysis provides evidence for simultaneous oil generation and expulsion from source rocks. Upon heating, kerogen decomposes to an expanding

tarry bitumen. The expansion causes the rock bedding plane to fracture, and this allows liquid oil to be expelled.<sup>8</sup>

Secondary migration refers to the movement of hydrocarbons from source rock to reservoir rock along a carrier system. The rate of secondary migration has been modelled at approximately 1 km/year; for those who believe in a deep time framework this would seem nearly instantaneous!<sup>9</sup> The style of secondary migration reflects the structural and stratigraphic framework of the fill of a basin. Vertical migration occurs mainly through faults and fractures that breach the seal, and is characteristic of petroleum systems in rift basins, salt dome provinces, wrench basins, fold and thrust belts, and deltaic sequences. In contrast, lateral migration requires a laterally continuous regional seal resting on an extensive permeable reservoir unit (that is, stratigraphically continuous seal-reservoir 'doublets') in a tectonically stable province, such as intracratonic platforms or foreland basins.<sup>10</sup> Australia's Gippsland Basin is an example where both generation and migration are believed to be occurring at the present time as carbonaceous source material (derived from algae and land plants) is exposed to higher temperatures by deeper burial.<sup>12</sup> It has been



**Figure 1.** A schematic to illustrate the main elements of a petroleum system. These elements are a generative source rock, migration pathway to a reservoir with overlying seal and a trap structure (such as this anticline) where petroleum accumulates. (After Craig and Quagliaroli.<sup>31</sup>)

concluded that the generated products migrated relatively rapidly either into traps or even to the surface.<sup>11</sup> It is therefore to be expected that many other areas are still generating oil, and it is actively migrating to traps even today.<sup>12</sup>

### Petroleum system sedimentation

With regard to deposition of sediments (source rock, reservoir, seal, and overburden are typically sedimentary), anti-creationist geologist Derek Ager said:

“Sedimentation in the past has often been very rapid indeed and very spasmodic. This may be called the *Phenomenon of the Catastrophic Nature of the Stratigraphical Record* [emphasis in original]”.<sup>13</sup>

Ager also emphasized that at particular times in Earth history peculiarly unique types of sedimentary deposition prevailed over vast areas of the earth’s surface, thus indicating that non-uniformitarian processes were at work.<sup>14</sup> Stratification experiments demonstrate that multilayered sediment packages can form laterally and rapidly by the action of currents. Sedimentary deposition studies show that duration of deposition is much less than indicated by the conventional geological timescale.<sup>14</sup> In addition, large marine transgressions and regressions can result from mountain-building events (orogenies) such as the Caledonian, Hercynian, and Alpine.<sup>15,16</sup>

The lithology of most petroleum reservoirs consists of three types: sandstones, carbonates, and combinations of sandstones and carbonates.<sup>17</sup> Depositional environments determine the basic architecture and geometry of sandstone petroleum reservoir rocks. Petroleum geologists have inferred that in non-marine settings, sandstone reservoirs are deposited in fluvial, lacustrine, and eolian environments, whereas in marine settings these reservoir rocks are in deltaic, shallow marine and deep marine settings.<sup>18,19</sup> Many fossil-containing carbonate deposits that were

once interpreted as fossilized reefs have been re-interpreted as debris flow or other non-reef structures that formed in a short timeframe.<sup>20</sup>

Vast and very short-lived blooms of calcareous algae (coccolithophores) have formed chalk deposits in modern times.<sup>21</sup> Thick Cretaceous beds of 98% pure calcium carbonate testify that they could not have been deposited over millions of years; otherwise the chalk would have been contaminated with sediments derived from continental erosion.<sup>22</sup> Coal is believed to represent fossil graveyards of plants transported by water and rapidly buried.<sup>23</sup> Cretaceous chalk petroleum reservoirs are found in the North Sea, the Gulf Coast, and Western Interior Seaway of North America.<sup>24</sup>

The seal rock is an essential element of the petroleum system, otherwise hydrocarbons would escape to the surface. Two important classes of seal are the regional seals, that roof migrating hydrocarbons, and local seals, that confine accumulations. The great majority of effective seal rocks are fine-grained clastics, organic-rich rocks, and salt- and gypsum-rich rocks.<sup>25</sup> Widespread Permian or Permo-Triassic salt and gypsum-rich rocks have sealed

Permian reservoirs and enabled the preservation of huge quantities of gas in Texas, the southern North Sea, North Germany, the Netherlands, and in southwestern Iran and other places in the Middle East. Gas tends to escape towards the surface, by means such as diffusion, so that preservation of such large accumulations requires an outstanding seal such as salt and gypsum-rich rocks.<sup>23</sup>

Tectonic events such as the formation of mountains and adjacent depressions, grabens, or otherwise subsiding areas are favourable for the formation of sedimentary basins and their various types of structural petroleum traps.<sup>4</sup>

Detritus derived from higher adjacent regions likely provided some of the stratigraphic fill for sedimentary basins and the petroleum and coal resources they contain. Basin subsidence curves are used by oil companies to try to get an idea of the relative order of subsidence and so temperature and petroleum-generation in sedimentary basins. The following example from the Sunda Basin, offshore Northwest Java, covers a radiometric age span of some 40 million years (figure 4). Current-day Jakarta, also in western Java, is observed to be subsiding at approximately 6 cm/year.<sup>26</sup> Extrapolated

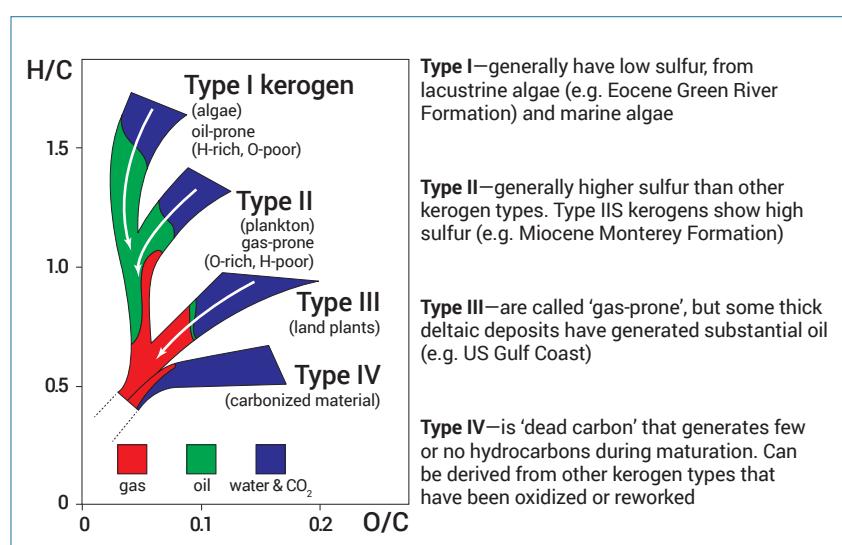
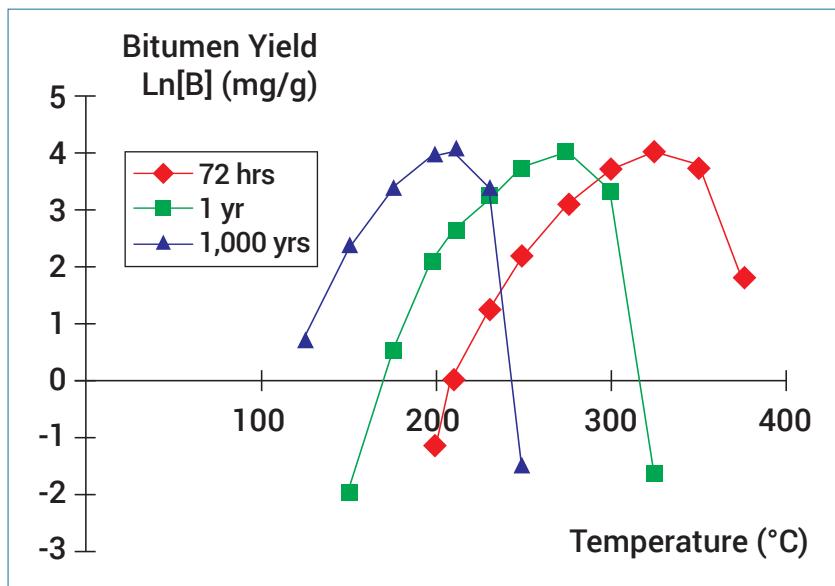
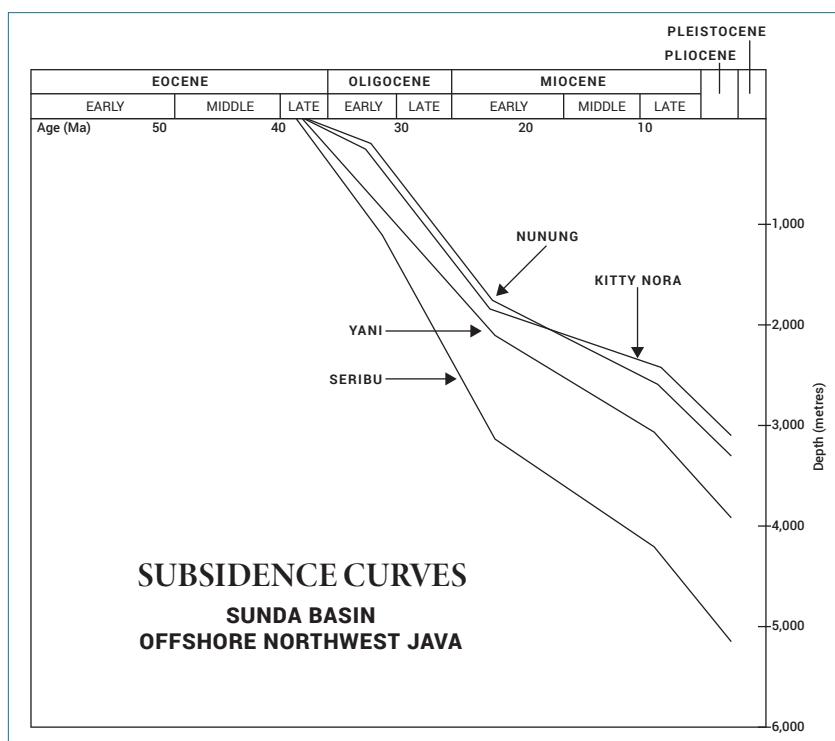


Figure 2. A van Krevelen diagram



**Figure 3.** Bitumen yield versus temperature for various times of heating based on the kinetic model of Nielsen and Barth.<sup>32</sup> After 1,000 years, significant bitumen can be generated within realizable temperatures in sedimentary basins. (After Bruce et al.<sup>9</sup>)



**Figure 4.** Subsidence curves of four well sections, Sunda Basin (after Koesoemadinata et al.<sup>33</sup>).

this would give a ludicrous subsidence depth of 2,400 km in 40 million years! Thus, even at some currently observed rates, basin subsidence does not need millions of years.

### Petroleum traps

Traps for petroleum can be divided into three main categories: structural, stratigraphic, and combination. Structural traps include anticlinal fold traps,

fault-associated traps, and piercement traps (such as salt domes).<sup>27</sup> The northern Perth Basin of Australia provides an example of hydrocarbon fields controlled by compressional anticlines in the lower Cretaceous, when Australia and Greater India were breaking apart.<sup>28</sup>

Stratigraphic traps, such as reefs and reef-like structures, permeability barriers in carbonate rocks, sandstone pinch-outs, and truncations are common in the large, relatively undeformed part of the North American platform. Discovery of these harder-to-find traps reflects the very mature and advanced state of exploration of North America compared to the rest of the world.<sup>23</sup> Stratigraphic traps require more intense exploration to define than the more simply configured structural traps.

### Oil preservation

Preservation versus degradation of oil is dependent on a number of factors and conditions, particularly the effects of certain types of bacteria. Oil can quickly decompose from bacterial action. The Deepwater Horizon rig's catastrophic blowout and oil spill on the Gulf of Mexico surface waters in 2010 is an example where small droplets of oil decayed within a year of washing ashore, broken down by sand-dwelling microbes. However, golf ball-sized clumps of oil (the most common size found along Gulf Coast beaches) took roughly three decades to decompose entirely.<sup>29</sup> Biodegraded oils are common in reservoirs around the world; for example, offshore Nigeria, the Middle East, Australia's Northwest Shelf, Western Siberia, the North Sea, the Gulf of Mexico, and China. Sixteen very large 'tar' deposits (that is, extremely biodegraded crudes) have been estimated to contain nearly as much heavy oil as the world's total discovered recoverable conventional oil reserves. Supergiant oil deposits are found in Western Canada and Eastern Venezuela foreland basins, where

there has been entry of meteoric water and oil migration for over 80 km.<sup>30</sup> Some non-biodegraded oils may be the result of recent recharge.<sup>18</sup> Some geologists who believe in deep time try to explain ‘ancient oil’ by a supposed process called ‘paleosterilization’ to prevent oil from biodegrading. They hypothesize that, if reservoir rocks exceed the threshold temperature of 80°C (176°F), bacterial action not only ceases but remains inactive for millions of years. However, there are thermophilic bacteria that thrive in extreme conditions such as hydrothermal vents on the seafloor.<sup>18</sup>

## Conclusions

The catastrophic nature of the stratigraphic record applies to sediments such as source rock, reservoir, seal, and overburden. The generation and primary migration of petroleum occurs rapidly under increased temperature conditions. Secondary migration under realistic conditions is also rapid. Tectonic activity during the Flood year and its aftermath could form traps very quickly. Modern oil spills demonstrate that biodegradation can occur within a short span of time. Hence the elements of, and the processes involved in, petroleum systems do not require deep time.

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# Post-Flood animals live above their dead Flood relatives

Michael Oard questions if Marcus Ross is right to conclude that North American mammals did not live above their dead Flood relatives.<sup>1</sup> The discussion is about whether the post-Flood boundary is somewhere beneath or above those fossils. If the boundary is beneath, that implies that God allowed huge watery catastrophes to create numerous fossils post-Flood. That also means that no fossils of those mammals were deposited in North America during the Flood. Both consequences are undesirable. I therefore am glad that Oard posits a much higher boundary. But I am missing the most essential and fundamental aspect. Wouldn't the Creator have had a plan by creating, flooding, and recreating?

Ecological zonation was almost certainly created in Creation Week.<sup>2</sup> So, as the pronghorn antelope was living in North America before the Flood, it is there where its fossils can be found.<sup>3</sup> And, after the Flood, the Creator brought the pronghorn antelope back to North America. It lives there today because it fits into His original plan.

So, in Creation Week, He created the animals to live in their specific biotopes. After the Flood, He recreated specific biotopes for them. He returned the animals from the Ark to their recreated habitats.<sup>4,5</sup> Because God is the same 'yesterday and today', He brought the animals indeed back "to their same continent of origin".<sup>6</sup>

Creationists may therefore continue to vigorously defend that the fossils and the strata testify to the Flood, just as the church has always professed.<sup>7,8</sup>

I don't want to play this card too dogmatically, as the Flood could have washed animals away, whereafter they became fossilized on different continents. Also, God could have decided to bring animals to different continents after the Flood for reasons unknown to us. I just want to prevent creationists from making too rigid, and probably false, conclusions by examining boundary-crossing taxa.

I would like to stress that it is perfectly reasonable that biogeography before the Flood would be identical to biogeography after the Flood. That animals now live on the layers of Earth containing Flood fossils of conspecifics is what might be expected.

Stef Heerema

Assen

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## » Michael J. Oard replies:

I thank Stef Heerema for his comments on my article. I agree that it is unlikely that huge post-Flood watery catastrophes would bury and fossilize tens of millions of mammals across the globe. As far as it being unlikely that Flood mammals would be deposited in North America, a closer look would show that many of these Tertiary Flood

mammals in North America are also found on other continents. So, it is no big deal for post-Flood mammals to have lived above these Tertiary mammals.

Ross had mentioned the pronghorn as being on North America in both Flood (Tertiary) and post-Flood time (Pleistocene). This is likely his best example. But I noticed Heerema called it an antelope, although the classification system does not. But the pronghorn is so close to an antelope that if we consider it an antelope, then they are found on all continents, except South America, in both the Tertiary and the Pleistocene. This would eliminate the uniqueness of North America.

I do believe in vertical and horizontal ecological zonation before the Flood, and animals were buried by habitat. However, I see no need to accept that God 're-homed' animals after the Flood at their pre-Flood locations. The mammals would have spread from the Ark, differentiating into various species, genera, etc. in the process. And I do not think that pre-Flood and Flood continents are necessarily the same.

Regardless, a closer analysis weakens Ross's argument that specific post-Flood mammals rounded the Bering Land Bridge, where winters would have been much warmer early in the Ice Age, and died over their pre-Flood ancestors from the Flood. Of more significance is, what were the kinds on the Ark, and how do they relate to the kinds before the Flood? I am still contemplating this issue.

Michael J. Oard

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# Rarity of long-lived post-Flood human fossils?

I read Robert Carter's article<sup>1</sup> on the apparent lack of evidence for long-lived humans with great interest. Even if the number of very old humans is necessarily a small percentage of the total population, I am pleased to suggest that evidence for long-lived humans may still be more abundant than his paper assumes.

A recent paper<sup>2</sup> notes that greater longevity has repeatedly been positively correlated with greater ages at maturity,  $t_{\text{mat}}$ , and larger adult body masses,  $M$ . And there is theoretical justification<sup>3</sup> to expect

$$M \propto t_{\text{mat}}^4 \quad (1)$$

The earliest age at which a Genesis 5 patriarch is listed as having a son is 65. Even if these listed sons are not first-born, these advanced ages strongly suggest that antediluvian humans were reaching sexual maturity at much

greater ages than extant humans. Likewise, the earliest listed age of a Genesis 11 patriarch on the birth of his son is 29, an age that today would be considered 'late' in life. Thus, it seems early post-Flood humans were also taking longer to reach adulthood. And eqn 1 suggests that this delayed maturation was tied to greater adult body masses.

Thus, evidence for giantism and delayed maturation are both evidences for greater longevity. Dr Carter mentioned Dr Jack Cuozzo's suggestion<sup>4</sup> that greater-than-expected wear on the teeth of Neanderthal children is evidence for delayed maturation.

There is both archaeological and cultural evidence that humans in the immediate post-Flood world were larger. A large 1997 study found that archaic *Homo sapiens* were 13–30% larger than modern humans.<sup>5</sup> Giant spear heads are on display at the Israel Museum (see figure 1).<sup>6</sup> Giant hand axes from Europe and Africa<sup>7–9</sup> seem too large to be practical<sup>10</sup> for today's humans, but they might have been useful to larger post-Flood peoples. Moreover, the wide geographical

distribution of these axes suggests that the use of such large tools was not restricted to giants living in the land of Canaan. Jewish legend says Adam was a giant, and some Flood legends suggest (if not state outright) that Noah and his wife were also giants and that humans became smaller after the Flood.<sup>11,12</sup>

Moreover, whatever factors caused human giantism/longevity would likely also have affected the animal kingdom. Thus, we might expect a post–Ice-Age size reduction in animal kinds that survived the Ice Age, and there is fossil evidence for this:

"Kurtén (1965) discovered that most carnivores in Israel and Lebanon underwent a considerable size reduction at the end of the Pleistocene. The dwarfing of fossil mammal lineages at the end of the late Quaternary was probably world-wide . . . [emphasis added]."<sup>13</sup>

Evidence for long-lived post-Flood humans (and animals) may be much more abundant than we have previously assumed. We just need to know what to look for!

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**Figure 1.** Copper spear heads, including a giant one (bottom row, fourth from left), on display at the Israel Museum, Jerusalem.

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» Rob Carter replies:

I read Dr Hebert’s letter with interest. The question of a possible delay in the time of sexual maturation among the Patriarchs has multiple ramifications and would influence, for example, population growth in the antediluvian and post-Flood world.<sup>1</sup> On another note, the ages at which sons are born are much less consistent in Genesis 5 than they are in Genesis 11. From Adam to Lamech (nine generations), the average age at the birth of the named son is 117.3 ( $\pm$  49.7 SD). From Arphaxad to Terah (seven generations), the average is 31.4 ( $\pm$  2.2) years. This might suggest that the list in Genesis 5 is a simple genealogy, while Genesis 11 is specifically a list of first-born sons. If Terah, the father of Abraham, was the oldest son in a line of inheritance stretching back to Shem, this might explain how the family records came into the possession of Moses (I assume Genesis was not dictated to him directly by God, but that Moses was working from source material, which was probably written, but perhaps oral). There may have also been cultural reasons for the men in Genesis 11 marrying about the age of 25 or 30, given that the first-born son in the line of Shem may have had some special status in the ancient world. In other words, even if 30 is the average age of marriage in this lineage, this

might not reflect the age of sexual maturation.

The question of how large people were in the past, however, is difficult to reconcile with the archaeological record. While human-made artifacts (bronze spear heads, etc.) are often larger than a normal human would find comfortable wielding, one could argue that many, or most, of these were for ceremonial purposes only. On the other hand, consider the Scottish claymore, a late-medieval, two-handed sword of huge proportions that was in use at the time as other soldiers were wielding much more slender, lighter, and shorter sabers. The claymore was a status symbol, but the fact that it dropped out of service shows how impractical it was. It may have required a strong man to use it properly, but many similarly strong men were not using them. Thus, the size of the weapon might not reflect the size of the man. Also, putting aside a handful of highly disputed remains that were discovered before the development of modern archaeology, there are no certifiable ‘giants’ in the archaeological record. We mention this on our list of *Arguments We Think a Creationist Should Not Use* page.<sup>2</sup> In fact, *Homo neanderthalensis*, *H. erectus*, *H. heidelbergensis*, etc., may have been ‘robust’, as opposed to the ‘gracile’ *H. sapiens*, but none of these were of giant stature.

Were ancient humans larger? Apparently, by some percentage. They were also more robust than the average person alive today. Yet, humans did not have the size variation that we see among many animals in the fossil record (e.g. giant glyptodonts vs. modern armadillos). Also, being that taller humans do not grow for more years than shorter people, there are genetic components to human height that are divorced from the age of maturation. Worse, among modern humans, there is a clear reverse correlation between height and age at death. Cancer, blood clots, and heart

disease are more common among taller people, simply due to their mass, and their average lifespan is shorter. Thus, a large average height among ancient people would counter the given biblical lifespans.

How does this all balance out? Nobody knows. Much more work needs to be done, in many different areas, before we can conclusively say much about the size, maturation time, or lifespan of early people.

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# One-way speed of light

I found the article in *Journal of Creation* 37(2) 2023 by Clifford Denton interesting and stimulating. I offer some more points for careful consideration.

For a rigorous proof that the two-way speed of light is constant we should also consider what happens when the apparatus moves at right-angles to the motion of light within it.

As seen in the absolute frame of reference of figure 1, the light in the apparatus will take a diagonal path of length  $L_1$  as it takes a time  $t$  for the downward journey.

The Lorentz transformation does not change  $L$ .

By Pythagoras,

$$\begin{aligned} L_1^2 &= L^2 + (vt)^2 \\ \text{So } (ct)^2 &= c^2 t^2 = L^2 + v^2 t^2 \\ \text{So } t^2 &= L^2/(c^2 - v^2) \\ (2t)^2 &= 4L^2/(c^2 - v^2) \end{aligned}$$

As the total time  $t_1 = 2t$ ,

$$t_1^2 = 4L^2/(c^2 - v^2)$$

The time  $t_2$  measured by the clock moving with the apparatus is  $\gamma t_1$ .

$$\begin{aligned} t_2^2 &= \gamma^2 t_1^2 \\ &= 4L^2(1 - v^2/c^2)/(c^2 - v^2) \\ &= 4L^2(c^2 - v^2) / c^2(c^2 - v^2) \\ &= 4L^2/c^2. \\ t_2 &= 2L/c \end{aligned}$$

Average speed apparent to the observer moving with the apparatus: total distance / total time, is

$$2L/(2L/c) = c.$$

This shows that the same average speed will be obtained whether the motion is parallel or perpendicular to the direction of the light, and also that in the latter case it is the same as the one-way speed. This is very satisfactory.

It is true that all the precise measurements of the speed of light have been two-way averages. However there are two groups of astronomical measurements, initially made about

three hundred years ago, which are difficult to interpret as two-way averages. Neither of them was planned to be a measurement of its speed.

## Ole Roemer

The first came from the very practical difficulty in the 17<sup>th</sup> century of determining longitude. Galileo had suggested that the eclipses of Jupiter's innermost satellite (which he had discovered, now called Io) could be used as a clock. Giovanni Cassini in Paris employed Ole Roemer to make accurate observations so that tables could be produced for this purpose. Roemer found that the timing of the eclipses varied with the distance of Jupiter from the earth, and eventually concluded that this was due to the time taken for the light to cross the orbit of the earth about the sun. There are times when the eclipses cannot be observed, such as when Jupiter appears close to the sun, and Roemer correctly predicted that after one such period in 1676 the eclipse would be seen some 11 minutes later than expected.

Roemer's conclusion was highly controversial in the 17<sup>th</sup> century. The eminent philosopher Descartes held that light travelled instantly, but Isaac Newton, Edmund Halley and Christiaan Huygens supported Roemer. Cassini remained sceptical but did include Roemer's adjustments in his tables as an empirical correction. With continual observations, they improved in accuracy (and user-friendliness).

In an edition c. 1730 the amplitude of Roemer's adjustment is 7 min (figure 2).<sup>1</sup>

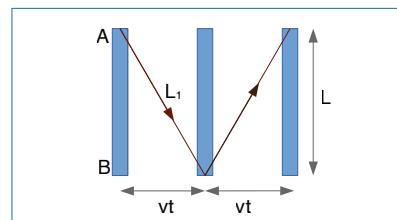
A sinusoidal adjustment implies that the speed of light is constant as it crosses the orbit of the earth.

These tables were accurate enough to be useful for surveying land. For example two observations made in 1730 in Beijing gave its longitude as 116° 13' and 116° 23' East of London. The accurate longitude is 116° 24' giving errors in position of only 10 miles and 1 mile respectively.

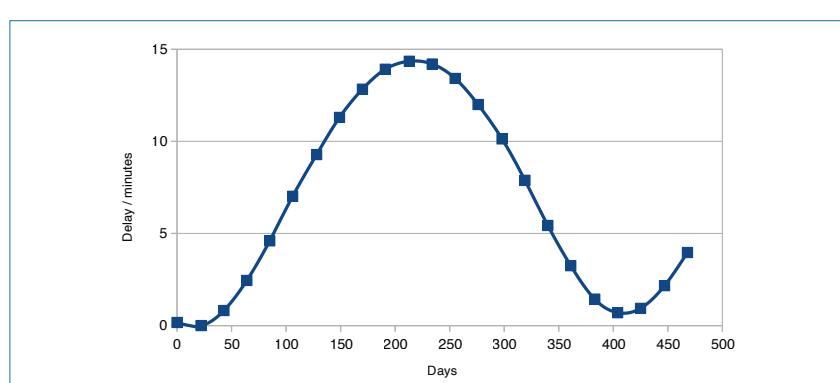
Sadly, this method failed for ocean navigation. It proved impossible to keep a 12-foot-long telescope (length recommended by Edmund Halley) steady enough on a ship to observe the eclipses.

## James Bradley

In the 1720s James Bradley was hoping to observe stellar parallax: an annual variation in the position of a star as it is viewed from the earth in different seasons. The angle (figure 3)



**Figure 1.** Apparatus AB moving at right angles to the light.



**Figure 2.** Roemer's adjustment included in Cassini's tables c. 1730

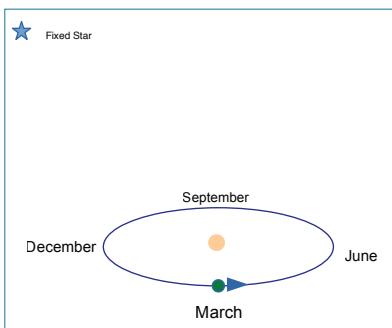


Figure 3. Orbit of the earth around the sun

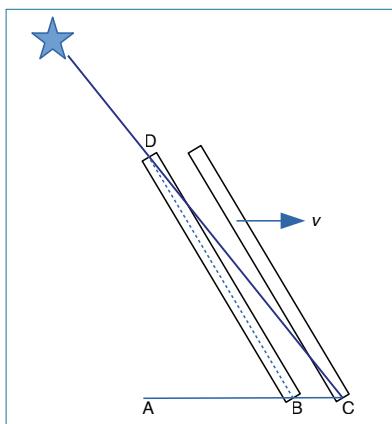


Figure 4. Bradley's explanation of stellar aberration observed through a telescope BD.

between the fixed star (which should be 1,000's of times further away) and the plane of the orbit of the earth should be largest in December and smallest in June.

What Bradley actually saw was that the angle was largest in March and smallest in September, three months later than expected. This was a great puzzle. Eventually he realised that the angle was greatest when the earth was moving fastest to the right, and smallest when moving fastest to the left.

Bradley explained that this ‘stellar aberration’ in March was due to the movement of his telescope from B to C (figure 4) in the time  $t$  it took the particle of light to travel from D to C. The telescope needed to be tilted at a steeper angle than the ray for the light to travel centrally down it.

$v$  = speed of the Earth.

$BC = v t$ ,  $DC = c t$ .

Let  $x$  = angle  $BDC$ ,  $y$  = angle  $ABD$ .

By the sine rule:

$$DC/\sin(DBC) = BC/\sin(x)$$

$$\text{Since } \sin(DBC) = \sin(ABD) = \sin(y)$$

$$c t / \sin(y) = v t / \sin(x)$$

$$c = v \sin(y) / \sin(x)$$

Over the course of two or three years, around 1727, Bradley observed the aberration of many stars. He found that the ratio  $\sin(y):\sin(x)$  was 10210:1 for all of them. At  $c = 10210 \times$  the speed of the earth, light could travel the circumference of its orbit in  $1/10210$  of a year, and its radius in  $1/2\pi \times 10210$  of a year which is 8 min 12 sec.<sup>2</sup> This was close enough to Roemer’s 7 min for light from the sun to reach the earth.

Bradley concluded that:

- Light comes at the same speed from stars in different positions in the heavens.
- Light comes at the same speed from bright stars and dim stars, which may be further away.
- Light from the sun, and light reflected (from Io) travel at the same speed.
- Copernicus was right to assert that the earth moved round the sun.
- The fixed stars are much further away than had been thought.<sup>3</sup>

Personally, I do not consider Post-Modernism to be a logical consequence of physical relativity. One could just as well say that a universal speed of light for all observers fits a universal standard of morality for all people.

Richard Ward

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2. The modern value is 8 min 20 sec, only 1.3% different.
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## » Clifford Denton replies:

I thank Richard Ward for his response to my article. He is correct that we need to deal with a system travelling at right angles to the emitted light if we are to consider the passage of light emitted at any and every angle to the direction of motion of the apparatus. This has a bearing, too, on the interpretation of the Michelson/Morley experiment, in which light was split into two directions at right angles.

It is most satisfying, as he says, how the results can be derived quite simply. Once one can adjust one’s mindset confidently back to absolute measurements, one makes progress. It is all too easy for one’s mind to be caught up in the fog that relativity theory has brought. That is why it was so pleasing to read Ward’s derivation of the parallel result, quite lucid and fog-free. It is my hope and prayer that others, more up to date with physics, will find this lucidity and take the work forward, especially where time dilation and length contraction can be investigated more fully.

We must continue to be rigorous with our work. It is all too easy to make logical errors, even though the mathematics is quite straightforward. In his own proof, Ward quotes the Lorentz transformation regarding length contraction. I would prefer to simply refer to length contraction and time dilation independent of Lorentz, because of the way time is tied up in the Lorentz equations as a variable. We can appreciate the work of others from the past, but seek right answers for right reasons rather than right answers for wrong reasons. We all depend on those who went before and enter the dialogue with humility, ever seeking to correct error.

Thanks also to Ward for the reminder of Roemer and Bradley. There is surely much that can continue to be investigated on the one-way passage of light.

Clifford Denton

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# Evolution as partner in evangelical academia?

**Science and the Doctrine of Creation: The approach of ten modern theologians**

Fulkerson, G.H. and Chopp, J.T. (Eds.)

IVP Academic, Downers Grove, IL, 2021

Benno Zuidam

**S**cience and the Doctrine of Creation advocates the compatibility of evolution and the doctrine of creation. This landmark coproduction of the Templeton Religion Trust, Intervarsity Press, and Trinity Evangelical Divinity School (TEDS) with an imprimatur by Alister McGrath is indicative of the state of neo-evangelical theology.

This volume seeks its inspiration and guidance not from Holy Scripture as the inerrant Word of God or the great orthodox theologians of the church, but from scholars like Pannenberg and Moltmann. This volume seeks its guidance for the doctrine of creation from theologians who not only deny the Trinity in any traditional sense, but the infallibility of Scripture as well. That these theologians operate from premises and arrive at doctrines that are at odds with a traditional definition of Christianity is not a hindrance. This is unfortunate.

## Disappointing

Personally, I was looking forward to reading this book, because the title suggested an overview of prominent theologians and perhaps an evaluation of their views in the light of Scripture and traditional doctrine. In that respect this book is somewhat of a disappointment.

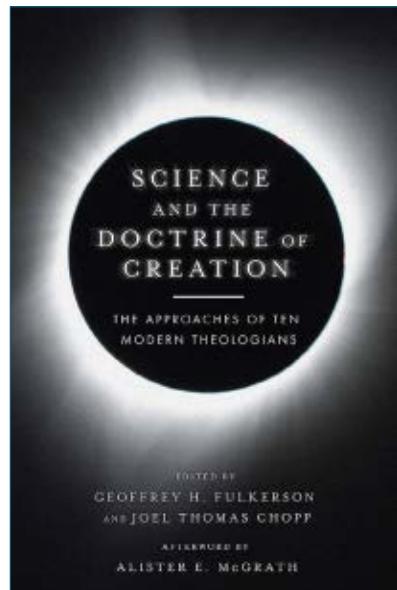
For instance, Schwöbel discusses Pannenberg's trinitarian views in neo-evangelical terms (p. 190), apparently without realizing that Pannenberg uses the term 'trinity' not in any orthodox sense at all.

Every chapter has a section that is supposed to be a neutral description of views, followed by 'a conversation with'. Often these two are mixed, while throughout *Science and the Doctrine of Creation* most contributing authors hasten to insist that the scholar whom they discuss puts nothing in the way of evolutionist science. The possible exception is Bradley Gundlach's chapter on Warfield, who insisted on mankind's unity in Adam, and the historicity of a worldwide Flood (p. 79).

## Evolution

Otherwise, the contributing authors in their own words:

- Fred Sanders: "On evolution, Pope accepts the idea of development broadly but contends that the very intricacy of the processes, to which the scientists rightly point, requires belief not in impersonal force, but in the personal God" (p. 28).
- Craig Bartholomew: "Kuyper is quite open to God having used evolution as his means of creating" (p. 50).
- Joshua W. Hipp: "There is in fact a deep concord between science and a theistic faith" (p. 96).
- Katherine Sonderegger: "There is one world and one truth, and the Lord God of all creation is the origin, the *ratio*, and the *scientia* of all that is. Such is the science I believe Barth would have welcomed" (p. 119).
- Kevin L. Vanhoozer: "Christ is the ground and grammar of the shared



intelligibility of theology and science" (p. 145).

- Stephen N. Williams: "As long as a theologian does not proceed in flagrant contravention of scientific knowledge or ignore prevalent scientific theory, we must surely be flexible in our expectations with regards to the extent and nature of the theologian's grasp of science. Theology has its own things to say just as science has its own things to say" (p. 167).
- Christoph Schwöbel: "Pannenberg attempts to show the compatibilities of scientific theories and theological reflection" (p. 189).
- Stephen J. Wright: "The Christian doctrine of creation, in Jenson's view, enables science by freeing us from the worship of the world" (p. 211).
- Murray A. Ray: "I have tried to show that the Christian doctrine of creation reveals the possibility, and indeed the necessity, of respectful collaboration between science and theology" (p. 240).

From the perspective of the Templeton Religion Trust (promoting multifaith and evolutionary science, templeton.org) one is tempted to respond: "Well done, ye good and faithful servants." Through its Covenantal

Pluralism Initiative, Templeton aims to promote religious freedom and literacy as well as the virtues of interfaith engagement across deep religious differences. It should be of concern to evangelicals that seminaries like Deerfield and Fuller and especially TEDS are collaborating with Templeton and accept grants for these specific purposes.

The absence of a modern theologian with genuinely orthodox positions on creation and science leaves the reader with the impression that any theologian who counted in the last 150 years was more or less open to the compatibility of Darwinism and the Bible, with the possible exception of Warfield.

### Kuyper misrepresented

Even Abraham Kuyper is presented as “quite open to God having used evolution as his means of creating” (p. 50). This is, however, a reinterpretation that dates back to the days of biologist and Vrije Universiteit Amsterdam (VU) professor L. Lever, who made Darwinism acceptable at the ‘Free University’. This view has been repeated by Abraham Flipse (e.g. *Annals of Science* 65(3):363–391, 2008). Insisting that Kuyper would have been open to God having used evolution is a way in which heterodox reformed scholars in the 1950s and ’60s tried to make their position acceptable by suggesting a continuity that never was. So general was the rejection of Darwinism at VU that it was only by 1933 that Professor Sizoo, classical scholar, dared to suggest reasons for contemplating an old earth. Bartholomew refers to the Kuyper lecture at VU (when he retired as rector) on evolution from James Bratt’s reader, which only comprises a part of the text in translation.

Had Bartholomew been in a position to consult the original Dutch in full (*Evolutie, Rede bij de overdracht van het rectoraat aan de Vrije Universiteit op 20 October 1899*,

Höveker & Wormser, Amsterdam 1899, pp. 1–51), then he would most likely have concluded with Koos van Delden (*Reformatorisch Dagblad*, 6 April 2006):

- a. Kuyper found Darwinism wanting in scientific respect and irreconcilable with purposeful creation, as he recognized that evolutionary theory does not allow for purposes, only for natural selection (p. 11).
- b. Kuyper pointed to the social implications of a scientific basis that considers survival of the fittest as a natural mechanism, and stated that this was completely unacceptable from a Christian point of view (p. 12).
- c. He argued that nature indicates that development from one proper species into another does not happen, and would lead to infertility if it did (p. 33).
- d. Fossil evidence for intermediate states between species are missing (p. 34).
- e. Breeding offers no experimental basis for Darwinism, as this only results in variation within the confines of a kind, not in evolution (p. 35).
- f. There is no evidence for spontaneous emergence of life (abiogenesis or chemical evolution) whatsoever (p. 36). Darwinism cannot explain our appreciation for aesthetics and any notions like beauty in nature (p. 39).
- g. Moral responsibility in the Christian sense and faith are clearly at odds with Darwinism and cannot have been the result of evolution (p. 41).

In sum, it is not a coincidence that Kuyper, on his retirement, chose to address the topic of Darwinism in his last rectoral address. With 40 pages specifically aimed at refuting evolution, Kuyper wished to impress on the next generation of leadership that Darwinism was at odds with orthodox Christian theology and should not be accepted.

Kuyper’s final words (in my translation) are as relevant today as they were in 1899:

“Dear Sirs, when I first stepped down as Rector, my warning was against the Criticism of Scripture, which stole from us the Revelation of our God. When I spoke of the ‘blurring of Boundaries’, I spoke against the murderous influence of Pantheism. I have now considered it my calling to raise my voice against the even more deadly danger lurking in Evolution. Not narrowly and for the Reformed tradition only, but for the sacred pledge entrusted to our Christian religion in its broadest conception, I have spoken both the previous times and also now. And so I also now end by seeking safety in what has always been and is and will be the foundation of the creed for the entire Christian church on earth, by maintaining against Evolution the first of all articles of faith: I BELIEVE IN GOD ALMIGHTY, CREATOR OF HEAVEN AND EARTH.”<sup>1</sup>

Kuyper stated unequivocally that, in his view, the first article of the Apostles’ Creed and Darwinism are enemies. Not partners in evangelical academia, as *Science and the Doctrine of Creation* suggests.

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1. Dutch original: “M. H., toen ik het eerst als Rector aftrad, ging mijn waarschuwing uit tegen de Schriftkritiek, die ons de Openbaring onzes Gods onstal. Toen ik over de ‘Verflauwing der grenzen’ sprak, nam ik het woord op tegen den moordenden invloed van het Pantheïsme. Thans achte ik het mijn roeping, tegen het nog doodelijker gevaar dat in de Evolutie schuilt, mijn stem te verheffen. Niet enghartig voor het specifiek-Gereformeerde, maar voor het heilig pand onzer Christelijke religie in haar breedste opvatting, heb ik én de beide vorige malen, én zoo ook nu, het woord gevoerd. En zoo eindig ik ook nu met mij terug te trekken in wat voor heel de Christelijke kerk op aarde in haar Belijdenis het uitgangspunt steeds was en is en zijn zal, door tegenover de Evolutie te mainteneeren het eerste van alle geloofsartikelen: IK GELOOF IN GOD ALMACHTIG, SCHEPPER DES HEMELS EN DER AARDE.” *Evolutie, Rede bij de overdracht van het rectoraat aan de Vrije Universiteit op 20 October 1899*, Höveker & Wormser, Amsterdam 1899, p. 45.

# Fine-tuned water

**The Wonder of Water: Water's profound fitness for life on Earth and mankind**

Michael Denton

Discovery Institute Press, Seattle, WA, 2016

Shaun Doyle

**T**he *Wonder of Water* is the second in Michael Denton's (currently) 5-book 'The Privileged Species Series'.<sup>1</sup> Denton is a Senior Fellow at the Discovery Institute's Center for Science and Culture and has an M.D. from Bristol University in the UK and a Ph.D. in biochemistry from King's College in London. He has also commented extensively on evolution, with influential books such as *Evolution: A theory in crisis*,<sup>2</sup> *Nature's Destiny*,<sup>3</sup> and *Evolution: Still a theory in crisis*.<sup>4</sup> In them, he showed that biology is pervaded by fundamental discontinuities that undermine the Darwinian expectation of a continuous spectrum of functionality between different types of organisms.

However, 'The Privileged Species Series' focuses on a different topic. It spells out the empirical fact of *fine-tuning*. There are many factors about our situation that have a 'Goldilocks' property. These are factors that, if they were even slightly different in any way from what they are, life as we know it would not be possible. In *The Wonder of Water*, Denton focuses on the many facets and functions of water that are 'just right' for human life (figure 1).

## Fine-tuned water—the science

Denton outlines his core thesis early on in the book:

"The one substance, water, is uniquely fit to serve two utterly

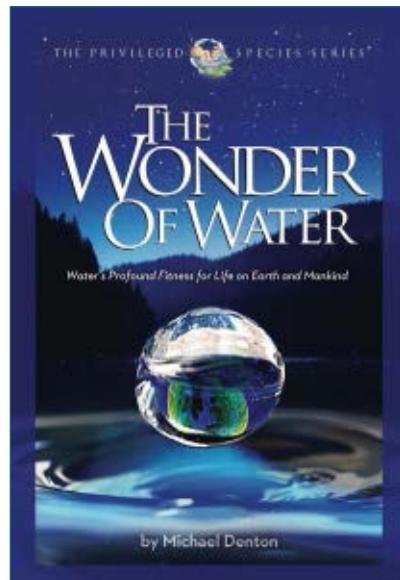
different vital ends—ends as different as can be conceived: the erosion of rock and the circulation of the blood. Both are absolutely vital to our existence. No other substance in nature comes close to having the essential set of properties needed to do these two jobs."

"If water served only these two very different vital ends, it would be miracle enough. But as we shall also see in the chapters ahead, water's unique fitness for life on Earth involves a vast ensemble of additional elements of fitness serving a vast inventory of diverse vital ends. These include the formation of the Earth itself, formation of the oceans, climate moderation and the hydrological cycle, tectonic plate movement, continent formation, and photosynthesis. The unique properties of water are also needed to make soil, cool the human body, fold proteins, and form cell membranes. Water enables phenomena and processes that unfold on vastly different spatial and temporal scales, from thousands of kilometers and millions of years down to nanometers and milliseconds" (pp. 9–10).

Water is a wondrous substance—it has a curious array of properties that make it uniquely fit for so many functions needed for life to exist and persist. It is impossible to mention them all, and some are more impressive than others. I will merely touch on some of the more interesting examples in the book.

## Water cycle

Consider the water cycle (figure 2). As it evaporates from the oceans and falls on the land as rain, snow, or hail, and eventually returns to the oceans via several different paths, several key properties unique to water mediate this.



First, it is the only naturally occurring substance on Earth that exists in three different phase states (solid, liquid, and gas) at ambient conditions (p. 13). Indeed, it has strangely high melting and boiling points for its low molecular mass. Why? Water forms many hydrogen bonds relative to its low molecular mass. Denton mentions two other properties of water crucial to the water cycle:

"Two more properties of water essential to the turning of the hydrological wheel are water's relatively low viscosity, and the relatively high mobility of liquid water compared with other fluids and of ice compared with many crystalline solids" (p. 16).

These properties prevent the excessive buildup of water and ice that would grind the water cycle to a halt. And Denton points out the consequences of water not having these properties:

"Without the hydrological cycle the entire land surface of Earth would be a dehydrated, lifeless waste, more lifeless than the Atacama or any of the most dehydrated deserts currently on Earth. Although the importance of the hydrological cycle is widely acknowledged, what is, as far as I am aware, never mentioned is the remarkable fact

that the delivery of water to the land, an essential medium of all life on Earth, is in effect carried out by and dependent on the properties of water itself, unaided by any other external regulatory systems” (pp. 16–17).

Without water having the properties it has, life on land would be impossible. Plus, water achieves this all by its own physical properties; it isn’t regulated by something else.

But not only is the delivery of water itself in the hydrological cycle important for life, so is its capacity to deliver the minerals life needs to thrive. As Denton points out:

“But what is really extraordinary about this second great function of the water wheel—that of delivering the minerals of life to terrestrial life—is the way in which a suite of diverse properties of water ‘conspire intelligently’ together to carry out the task of eroding and weathering the rocks” (pp. 17–18).

What factors are these? They include: water being a solvent of diverse compounds, its high surface tension, the fact it expands upon freezing, and how water supports ice movement.

Most interesting, though, is the way water’s diverse properties work together to achieve several different ends.

“The intelligent collusion of various diverse properties of water to serve a particular end such as observed in the erosion and weathering of the rocks, which might be loosely termed ‘teleology in parallel’, is not the only type of teleological pattern of synergic interactions manifest in the unique properties of water for land-based life. This is when one unique property of water—such as water’s ability to exist in three states of matter, enabling the hydrological cycle—must be causally prior to the exploitation of a second set of properties—such as those involved in the erosion and weathering of the rocks—which are in turn logically prior to and necessary for



**Figure 1.** Water gives us ‘just right’ conditions for the existence and persistence of life on Earth.

a third—such as the water-retaining properties of soil. Such a purposeful use of various elements of fitness in a logical sequence represents what is in effect a teleological hierarchy” (p. 33).

Water does not just have a bunch of goldilocks properties that make it useful for these diverse ends. More than that, these ends are themselves linked together by the properties of water in a logical order of explanation. It bespeaks a structural complexity to the system that permits the existence of life that, in our experience, reflects the highest forms of intelligence to accomplish.

#### Photosynthesis

Photosynthesis is one of the most important processes needed for life to persist on this planet. However, it depends on a minuscule proportion of light compared to the wavelengths available in the cosmos. Denton elaborates:

“As I pointed out in *Nature’s Destiny*, ‘The wavelength of the longest type of electromagnetic radiation is unimaginably longer than the shortest by a factor of  $10^{25}$ , or 10,000,000,000,000,000,000. Some idea of the immensity this figure represents

can be grasped by the fact that the number of seconds since the formation of the earth, 4 billion years ago, is only about  $10^{17}$ .<sup>5</sup> So how much of that real estate is visible light? ‘If we were to build a pile of  $10^{25}$  playing cards, we would end up with a stack stretching halfway across the observable universe,’ and the visual region would be ‘equivalent to one playing card’ in that stack” (p. 130).

It’s impressive enough that around 70% of the sun’s radiation is output in the visible range (p. 131). But what is most surprising is the ‘coincidental’ way water absorbs practically all light *except* visible spectrum light, allowing for photosynthesis to occur:

“These considerations of the immense range of EM radiations and the tiny region fit for photobiology brings us to perhaps the most dramatic manifestation of water’s unique fitness for life discussed so far: Water strongly absorbs electromagnetic radiation in every region of the spectrum *except* for the visible region, the only region in the entire spectrum useful for photobiology. Water, in one of the most staggeringly fortuitous coincidences in all nature, lets through only the right light in

an infinitesimally tiny region of the EM spectrum—the one playing card in the stack of  $10^{25}$  stretching half way across the universe” (pp. 131–132).

#### Perspiration

Who are the best distance runners in the ‘animal kingdom’? Especially when the going gets hot? We may not be the absolute best (e.g. ostriches, camels, and horses), but humans come pretty close. Part of it has to do with our upright, bidepal morphology, which is more energy efficient for long-distance running than four-legged locomotion. However, a prominent reason has to do with our body’s cooling system: evaporative perspiration. What makes this so efficient at keeping us cool is water’s anomalously high latent heat of vaporization—40.66 kJ/mol (2,257 kJ/kg)—higher than almost any other substance, and higher than any other molecular fluid.<sup>6</sup> This means that a gram of water that evaporates from our skin can carry away more of excess body heat than a gram of any other molecular fluid. So, of the relatively few substances that exist in abundant quantities as both a liquid and a gas under ambient conditions, water is the best for cooling.

Humans exploit this more than animals do. Denton points out that we can do this more effectively for long periods in the hot equatorial sun than other mammals, like dogs and deer, since we are not covered with hair or fur anywhere as thick as they are (pp. 145–146). Moreover, of the three main ways for our bodies to lose heat: conduction, radiation, and evaporation, evaporation becomes more relevant as air temperatures approach our body temperature. And evaporation is the only one that works above our body temperature. As Denton sums up:

“The high latent heat of evaporation ... reveals a fitness of water for warm-blooded terrestrial mammals and birds living in regions where temperatures are often over 30°C

(most of the globe) and where they often approach 37°C (many tropical regions and deserts). But because of our relatively minimal body hair and copious sweat glands, it is arguably of more use to humans than to any other organism on Earth. That this unusual property of water is particularly useful to us is one more indicator that water is uniquely fit not just for warm-blooded terrestrial organisms, but especially for humans” (pp. 148–149).

#### Fine-tuning in old-earth context?

The most objectionable part of the book from a biblical point of view is how Denton problematizes some of the issues in the context of deep time. For instance, how he prefaces the importance of water to tectonic recycling:

“Without continual renewal of the mineral content of the oceans, the oceanic ecosystems would grind to a halt in a few million years and the Earth’s oceans would become lifeless. Yes, the oceans receive nutrients from continental runoff, but there is not enough runoff, not enough continental landmass, to keep up with the rate of depletion.

“And yet over many hundreds of millions of years, the oceans have not been rendered lifeless, nor the mountains ground into sterile plains. But how could there have been continents and mountains and life on land for 400 million years? And how could there have been life in the seas for four billion years? What mechanisms are continually remaking mountains and replenishing the mineral content of the ocean waters?” (p. 40).

Plate tectonic recycling is the ‘solution’ to the ‘problem’, and water is the key that makes tectonic recycling possible.

What are we to make of this? Do we reject his solution and embrace

his problems as genuine problems for deep time? I think that is likely in some cases. In some cases, his solution might create problems of its own. For instance, even if the continual production of new continental crust can explain why it can persist for billions of years, it seems harder to explain why particular pockets of continental crust can survive for over 3 billion years if erosion would level all the continents in 10–50 million years. Moreover, there appears to be a problem of not enough sedimentary rocks given deep time,<sup>7</sup> especially if the continental crust is as stable as its radiometric age profile suggests. Moreover, problems such as the faint young sun paradox<sup>8</sup> and the moon’s recession rate from the earth<sup>9</sup> cannot be solved simply with recourse to the properties of water. Indeed, they require naturalistically improbable ‘Goldilocks’ conditions of their own to render them compatible with the standard deep time narrative.

However, when we actually pay attention to what Denton is saying in these instances, we realise some of these arguments may still have much value. Why? The points he makes are about how water enables processes to sustain the planet as life-conducive over billions of years and show no signs of waning. The irony here is that the longer the world can sustain such a fine-tuned condition, the more impressive a feat of engineering it appears to be. In other words, deep time works *against* the naturalist.

But if some of Denton’s arguments are successful in a deep time context, does this pose a problem for biblical creation? No. Such notions can be incorporated into a biblical creationist model of Earth history if they are found to be successfully functional. For instance, consider the notion that Creation Week, the Flood, or both involved God finely tuning those events to produce (or continue, in the case of the Flood) a dynamic life-sustaining Earth system that can persist

almost indefinitely. In other words, the system is design parameterized to be a functionally mature self-sustaining system. The notion that it's fine-tuned to run for far longer than it has run is irrelevant to how long it actually has run.

### Fine tuning and explanation

Denton is characteristically shy about inferring design:

“Whether the remarkable instances in which various properties of water work together to serve a vital end ... are actually the result of design or not, there is no doubt that they convey a compelling impression of design” (p. 216).

Nonetheless, he does a good job of underscoring the problems of avoiding teleology. He deals with ‘bad design’ objections by pointing out that water, since it performs so many different operations, is subject to constrained optimization. Thus, while a particular molecule might outstrip its fitness for use in one particular area (e.g. its ability to act as a broad-spectrum solvent), it fails in other areas (e.g. molecular weight or relative abundance). Water is not a ‘one trick pony’; its fitness for use as life’s liquid medium is based on many different properties that enable it to fulfil myriad roles.

Moreover, many of the ‘bad design’ arguments against water stress the problems it creates for the origin of life. As Denton admits, however, there is no agreed upon take for the naturalistic origin of life. In fact, he turns the problem around on the skeptic:

“Moreover, at least some stages in the origin of life must have occurred in an aqueous environment; and if some researches are to be believed, the provision of proton flows, a process unique to water ... , may have played a critical role” (p. 218).

Nonetheless, the biggest problem with this objection is that it assumes

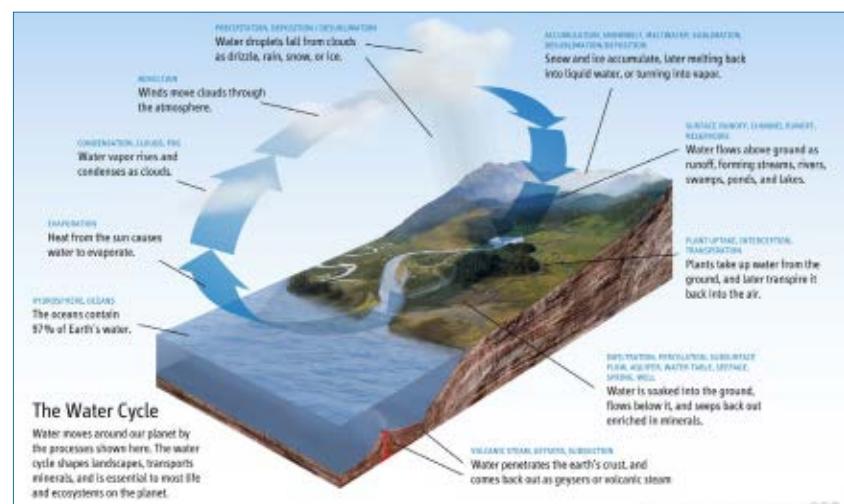


Figure 2. The water cycle

Image: Ehud Tal, Wikimedia / CC BY SA 4.0

abiogenesis. If an intelligent agent designed life, then these issues are moot.

So, Denton entertains the design explanation and notes its intellectual strengths. He does not, however, assent to it himself. He opts for a more modest conclusion:

“The unique fitness of nature for life on Earth and for beings of our biology, manifested so spectacularly in the properties of water, is a scientific discovery, whatever the ultimate cause of that fitness may be, whether by design or not.”

He does think, however, that the fine tuning of water for human life shows that we are not a purposeless accident:

“The properties of water show that beings with our biology do indeed occupy a special central place in the order of nature, and that the blueprint for life was present in the properties of matter from the moment of creation. We may have been displaced from the spatial center of the universe but not its ‘teleological center’” (p. 10).

This is good as far as it goes, but it does not go far enough. Denton stated elsewhere that his preferred explanation is “internal causal factors according to a structuralist ‘laws of form’ framework”.<sup>10</sup> However, this is

not only inconsistent with Scripture, it is contrary to common experience. We have no knowledge of such ‘laws of form’ that can give rise to teleology. We are, however, thoroughly acquainted with intelligent agency. Indeed, it’s the only form of teleology we are familiar with in ordinary experience. So, why deny that the sort of multivalent and directionally ordered fine tuning Denton documents so well for water is God’s handiwork?

### Assessment

Denton’s argument has weaknesses. He clearly supports deep time, and in some cases ties his argument closely to deep time. This can tie it closely to naturalism. Moreover, he’s shy about inferring a designer, and prefers to talk more broadly of teleology. As such, readers should read his arguments with care.

Nonetheless, there are some interesting ways the argument can benefit the biblical creationist. Since he problematizes his arguments in the context of deep time, that can reveal potential problems with deep time. However, it can also reveal some interesting ripostes to naturalists for creationists to exploit.

But it's in what we see in the science of water that this book shines brightest. The science of water itself, and how it is so functionally fine-tuned not just for life. Not just for terrestrial life. Not just for rationally reflective terrestrial life. But for *humans*. Creatures with our mentality *and* morphology that are capable of building the wonders of modern technological society.

### Conclusion

As with *Fire-Maker*, *The Wonder of Water* is a *tour de force* in the science of fine tuning. For that alone the book is well worth the read. And it reveals what may be perhaps one of the most compelling reasons to challenge skeptics: with all this fine tuning around us, how can you be so sure that we're nothing more than a cosmic accident? But we should push beyond this. Not only is it problematic for atheism, it's what we expect from Scripture. It doesn't just point to purpose *per se*. It points to God's purposes *for us*.

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# The fantasy world of eugenics: then and now

**Control: The dark history and troubling present of eugenics**

Adam Rutherford

W.W. Norton & Company, New York, 2023

*John Woodmorappe*

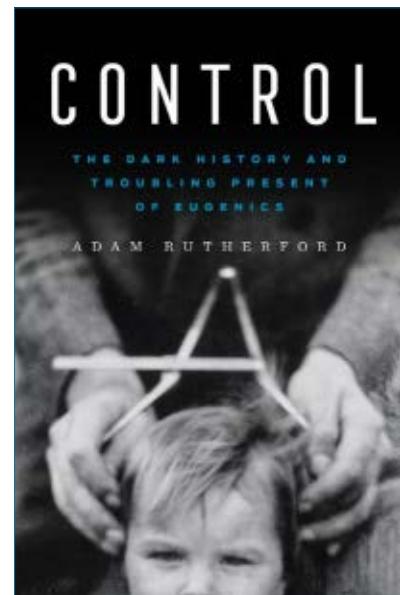
**A**uthor Adam Rutherford is a London-based geneticist and author of several books. He appears frequently on British television. His book provides a detailed history of the eugenics movement.

Throughout this book, Rutherford displays a pronounced bias as he repeatedly invokes the presumed danger of white nationalism. This undoubtedly colours his view of eugenics as primarily a tool to advance white supremacy at the expense of non-white peoples. Despite his questionable objectivity, I focus on worthwhile information that he presents.

This book has limited direct relevance to the creation–evolution issue. Rutherford conspicuously pays little attention to the role of the Darwinian revolution in creating and enhancing eugenics, even though this role was considerable (figure 1).

### No Christian bashing

The author is clearly an atheist; he uses a small ‘g’ when mentioning the God of the Bible (p. 25). Despite being an atheist that disparages the God of the Bible, Rutherford shows an element of fairness to Christianity. He realizes that some Christians supported eugenics while others did not, just as some Christians supported



slavery while others did not (p. 81). This corrects those who simplistically bash Christianity for its onetime support of this or that. Indeed, as Christine Rosen documented in her 2004 book *Preaching Eugenics*, the liberal churches that rejected biblical authority were on the then trendy eugenics bandwagon. The only real opposition came from conservative Evangelical and Catholic churches.<sup>1</sup>

### Science is not objective, value-free research

As noted earlier, the author does not touch on creationism or Intelligent Design. However, he inadvertently alludes to the fact that those scientists that scorn these positions as illegitimate are the pot calling the kettle black. He writes:

“However, all science is political. This is a statement that causes vexation among some who confuse the ideals of science with its

reality . . . Sometimes the biological and the political are deeply intertwined . . . Our fundamental biology is not isolated from the architecture of our societies, nor has it ever been” (pp. 5–6).

### On being gay

Rutherford has a mixed view of homosexuality. On the one hand, he endorses the view that 10% of people globally are gay (p. 33). This guesstimate is much higher, even by multiples, than most other ones. On the other hand, he rejects the usual politically correct orthodoxy that being gay is genetically inevitable and that it is unchangeable. He makes these candid remarks:

“Some people change their sexual preferences during their lives . . . There is a genetic component to sexual behavior and that includes homosexuality, but those genes don’t make you gay” (p. 214).

That is a no-no. According to the politically correct Newspeak, we are supposed to say ‘sexual orientation’, and never ‘sexual preference’, because the latter implies a choice, which the gatekeepers do not want us to consider.

### Many victims of Nazi German racism

Most scholarly and educational materials focus almost exclusively on the Jews. In contrast, Rutherford realizes that there were many victims as a result of Nazi German philosophy and policies. With reference to the ‘Permitting the destruction of lives unworthy of living’, he comments:

“That term—*Lebensunwertes Leben*—would develop over the next few years to be central to Nazi euthanasia and eugenics, and comprised the generically mentally ill people, people with disabilities, alcoholics, homosexuals, interracial couples, criminals, and people

who were sources of ‘social turmoil’, which would eventually include Jews, Slavs, Roma, Jehovah’s Witnesses and other ethnic or religious groups” (p. 118).

### Eugenics did not cause the Holocaust

Unfortunately, Rutherford advances the misconception that the Holocaust itself was the product of eugenic thinking. He believes that

“Very obviously, the largest part of the Holocaust was an intention to purify the Nordic race. This was folly squared, because there is no Nordic race, and there is no such thing as racial purity” (p. 215).

The truth about the Jews is otherwise. Nazi racial policies called for the segregation of Jews from the rest of German society. However, the physical extermination of Jews arose from an entirely different consideration. Hitler plainly warned, in early 1939, that if ‘international Jewry’ caused another world war, he would destroy all of Europe’s Jews in retaliation. This became reality in late 1941, when the USA entered the war against Nazi Germany at the behest of Jewish influence (in Hitler’s mind).

Of course, eugenic killings had given the Nazis plenty of practice in killing unwanted peoples.

### Even in its heyday, eugenics directly harmed relatively few people

The Nazis killed tens of millions of people overall. However, those killed for obviously eugenic reasons (such as through Aktion T4), took the lives of ‘only’ 300,000 people (p. 127). It also appears that the effects of eugenics on American policy have been way overblown. Some 70,000 people were sterilized since 1907 (p. 147). This is a drop in the ocean

compared with the size of the entire American population.

### Eugenics is not the tool of white supremacy after all

The author alleges that whites felt threatened by the gains made by non-whites and, for this reason, invented eugenics. He finally admits that eugenics had a broad appeal, and that this broad appeal went far beyond trying to guarantee the supposed white privilege over non-whites. He writes:

“Many playwrights, suffragists, philanthropists and philosophers, as well as more than a dozen Nobel Prize winners, embraced the ideas of eugenics as a force to change society, some with an almost religious fervor” (p. 10).

So changing society was the issue, not white supremacy.

Nor was eugenics the sole provenance of reactionaries. It was also embraced by progressives, who were supposed to be the paragons of enlightenment. Rutherford comments:

“It is appealing to think that the eugenic maintenance of existing power structures in Britain was solely the preserve of right-wing ideology, but this was not the reality. . . . The reduction of poverty via coercion or compulsory sterilization was not anathema to the socialism of prewar Britain; it was part of it. . . . Many of the founders of the influential left-wing think tank the Fabian Society were eugenics fans . . . ” (pp. 86–87).

The final proof that eugenics is not the product of white supremacy is evidenced by the fact that non-whites also practice eugenics. For instance, the Chinese (92% ethnically Han) not only oppress the Uighurs, but also reportedly practice sterilization on them (p. 149).

## Eugenics will neither lead to a utopia nor a dystopia in the foreseeable future

People commonly fantasize scientific progress eventually creating a world of perfect, tailor-made humans, or, alternatively, a world of slaves that have been genetically modified to make them totally unquestioning and servile. Rutherford rejects all such forms of utopias and dystopias. He contends that, even today, the making of tailor-made humans of any kind is unrealistic. He comments:

“The progress we have made in genetics since then [the Nazi era] has been spectacular, and in the last few years the pace has accelerated magnificently. But it is my contention that with our knowledge of human genetics as it currently is, the eugenic visions of Galton, Ploetz and Davenport are not much more realistic than they were a century ago. The complexities revealed in the thronging networks of endless genetic variants in human beings make selection for many of the

traits targeted in the past *harder* to understand than in those pre-molecular days. If we were to enact eugenics policies today, would we really know what we are selecting for or against? [emphasis in original]” (p. 233).

## Were it possible, would we even want a world of ‘perfect’ humans?

The essence of eugenic thinking is the improvement of the human race. Let us look at this more closely. Rutherford points out that, had the eugenics laws made in the United States and Germany been practised more widely and into modern times, humanity would have been robbed of talented people such as Woody Guthrie, Robin Williams, and many others. Had their embryos been ‘tweaked’ to correct their ‘defects’, their talents may never have emerged.

The author extends this reasoning: “Maybe we might wander beyond the realm of known diagnoses and come to the realization that some of the more colorful

characteristics of much loved historical figures were actually undiagnosed conditions that an alternate eugenic timeline might have precluded their being. Maybe Beethoven would never have existed ... [nor] Isaac Newton ... Abraham Lincoln” (p. 234).

Parenthetically, all this has unmentioned theological implications. Apart from considering the effects of the Fall, it helps us understand why God allows people to exist that have disabilities. No human being is a ‘mistake’. Every kind of human has worth, and every human has a contribution to make to humanity.

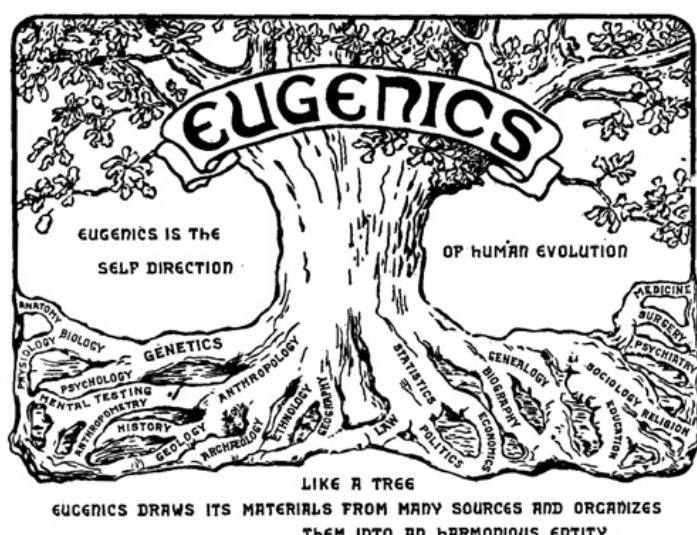
## Conclusions

Author Adam Rutherford’s closing statement provides the most resounding conclusion, “Eugenics is a busted flush, a pseudoscience that cannot deliver on its promise” (p. 239). It is important that we not live in a fantasy world where ‘perfect’ humans can be made, thanks to scientific progress. It is also important that the history of eugenics, along with the history of many other events, not be weaponized for use in order to advance any ideology that is currently in vogue.

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Image: Harry H. Laughlin, Wikimedia / Public domain



**Figure 1.** Although hardly mentioned in this book, the support Darwinian evolutionary views gave to eugenics was considerable.

# An evolutionist guide to the supposed hominin fossils

**The Human Lineage, 2nd edn**

Matt Cartmill and Fred H. Smith

John Wiley & Sons, Hoboken, NJ, 2022

Peter Line

This is the second edition of *The Human Lineage* by the authors. The first edition was published in 2009. Matt Cartmill is Professor of Anthropology at Boston University and Professor Emeritus of Evolutionary Anthropology at Duke University. Fred Smith is University Professor Emeritus of Anthropology at Illinois State University and Adjunct Professor at the University of Colorado. The blurb on the back of the book describes it as a “comprehensive textbook”, “the best and most current guide to the morphological, geological, paleontological, and archeological evidence for the story of human evolution.” It is said to cover “the entire story of human evolution from its Precambrian beginnings to the emergence of modern humanity”, and to be “indispensable reading for all advanced students of biological anthropology.” My detailed assessment of many of the supposed hominins (i.e. fossils believed by evolutionists to be human ancestors and/or more closely related to humans than to chimpanzees) is published elsewhere.<sup>1</sup>

The main body of the book is organized into eight chapters (excluding foreword, prefaces, notes, appendix, bibliography, and index), consisting of 469 pages of text, figures, and tables. With large page size and small text font, it is a comprehensive overview,

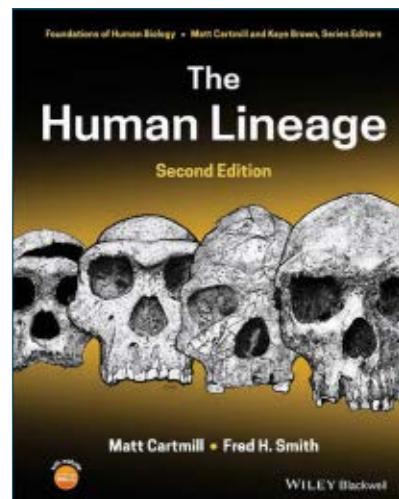
covering most of the important supposed hominin discoveries. The book contains many useful tables and illustrations, with most of the latter drawn by one of the authors (Cartmill). In the words of the authors, they use

“... informal, taxonomically non-committal labels for groupings of fossil hominins that are often described as species but that we suspect may be semispecies, multiple species, or vaguely defined chronospecies: Afarenses, Ergasters, Heidelbergers, Neandertals” (p. xx).

In many ways, using these added terms adds even more taxonomic confusion to an already perplexing situation. I will therefore try to avoid using these terms as much as possible, and stick to conventional species names (e.g. *Australopithecus afarensis*, *Homo erectus*, *Homo heidelbergensis*, etc.), though in some instances the author’s terms are difficult to avoid.

## The fossil record

In chapter 1, it is claimed that “the sacred poetry of the Hebrew scriptures, in which the voice of God from the whirlwind reproves would-be geologists”, constrained speculation about the history of the earth throughout most of the history of Western thought (p. 1). This early attack on the creation story in Genesis leaves little doubt as to what sort of interpretation lenses the authors use throughout the book. This chapter includes a discussion of various dating techniques, including some of their limitations, but accepts their validity. Coverage of the problems, flawed assumptions, and unreliability of age-dating methods, with emphasis



on radiometric dating, is available elsewhere.<sup>2-4</sup>

The authors admit that it “is not clear how instructions for making the proteins needed to make DNA could have become encoded in a DNA molecule” (p. 12). The reality is that naturalistic origin-of-life scenarios, which attempt to show how a first self-replicating cell could have been created by unguided and unintelligent processes (i.e. by chance), are thoroughly discredited.<sup>5,6</sup> Leaving aside this giant problem, the rest of the first chapter involves speculations on how life is supposed to have subsequently evolved, from allegedly around 4 Ga ago up to the arrival of mammals. As such, these evolutionary speculations, including the ones in the chapters that follow, are espousing a belief system (some would say religion) called ‘scientism’. Scientism is described as “... a scientific worldview that encompasses natural explanations for all phenomena, eschews supernatural and paranormal speculations, and embraces empiricism and reason as the twin pillars of a philosophy of life appropriate for an Age of Science.”<sup>7</sup>

Hoping against hope that a naturalistic origin-of-life explanation will somehow be found in the future is

not exactly an embrace of empiricism and reason.

### Analyzing evolution

Chapter 2 discusses Darwin's theory, speciation, species, classification, microevolution and macroevolution, phylogenetics, and other concepts as they relate to evolution. Here, the authors reveal themselves to be lumpers (as opposed to splitters) regarding defining species. Lumpers believe "it is better to recognize as few species as possible" (p. 40).

However, no attempt is made to address the insurmountable problems with evolution theory, which renders human evolution impossible from a scientific viewpoint.<sup>8</sup> One fatal problem is the waiting time problem; that is, it takes too long for specified DNA mutations to become fixed within a so-called hominin population.<sup>9</sup> Another catastrophic problem is that the genome has been deteriorating (due to accumulation of genetic mutations) ever since its origin, and the rate of deterioration cannot explain the preservation of information over timespans of millions of years.<sup>10</sup>

Throughout the book, independent evolution, i.e. parallel evolution as well as convergent evolution, is used in discussions to explain similar features that cannot be explained by a common ancestor. However, the vanishingly small probability of a feature evolving even once, let alone multiple times, is ignored.

### Primates

Chapter 3 includes discussions on the supposed first mammals, allometry in mammals (how body proportions and ratios change with body size changes), and what a primate is. An overview of living primates, as well as outlining anatomical differences in the skulls of humans and apes, is given. Also discussed is a speculative account



**Figure 1.** A cast of the *Australopithecus africanus* juvenile Taung 1 skull from South Africa (discovered in 1924). It consisted of a partial cranium, mandible and natural endocast. Photo: Peter Line.

of the primate fossil record, in terms of alleged evolutionary history, from the supposed stem group to Miocene apes. Rather than forcing a fictitious evolutionary tale on the fossils, one could simply say that extinct primates varied as do living primates.

### Australopithecines

For those interested mainly in the supposed fossil hominins, chapter 4 is where it all starts. This chapter summarizes most of the major fossil finds of the so-called hominins not usually assigned to the genus *Homo*. As such, the focus is on the australopithecines, but not exclusively so. In my view, the australopithecines were simply an extinct apish primate group. The almost obligatory story of the Taung child (figure 1) is rehashed for the umpteenth time in evolutionary literature, early in the chapter, and the reader will be spared further mention of it here.

In discussing the anatomy of bipedality, the authors curiously state that "the human lower back is not much of an advertisement for intelligent design" (p. 116). In a cursed world our bodies do not always

work optimally, but this is hardly an argument against it being designed.<sup>11</sup>

The authors lump the genus *Paranthropus* (i.e. the robust australopithecines) into *Australopithecus* (p. 129). Concerning the oldest 'hominin' contender, *Sahelanthropus tchadensis*, the authors conclude their analysis of this find by stating:

"In view of the shattered and deformed condition of the skull, and the conflicting claims that have been published about the stratigraphic context of the *Sahelanthropus* finds ... many paleoanthropologists are suspending judgment on the significance of these fossils until more specimens are found" (p. 140).

Three contenders vie for the title of 'first hominin': *Sahelanthropus tchadensis*, *Orrorin tugenensis*, and *Ardipithecus kadabba*, with considerable disagreement between proponents as to who wins the 'honour' (p. 146). However, the authors write that

"None of these disputes can be settled until we know for sure whether these Late Miocene hominids represent three different species, let alone three different genera" (p. 146).

This last sentence in many ways sums up the state of play regarding much



**Figure 2.** Cast of the adult KNM-WT 40000 *Kenyanthropus platyops* cranium from West Turkana, Kenya (discovered in 1999). Photo: Peter Line.

of the alleged hominin fossil record. There are disputes over anatomical reconstructions, dating of specimens, interpretations, classifications, etc. The tale of human evolution has changed numerous times, sometimes at the drop of a dime, and seems to be the only thing ‘evolving’.

The fossils attributed to *Australopithecus anamensis* are said to be the “oldest fossils that all experts acknowledge as hominin” (p. 146). *Australopithecus afarensis* (e.g. the famous ‘Lucy’) is presented as a species in a ‘classification muddle’ (p. 152), mainly because of a find known as the Burtele foot. The latter had a grasping, hand-like foot, like *Ardipithecus*, but supposedly lived a million years later, at the same time and place (Ethiopia) as *A. afarensis* (pp. 146, 152). The authors cite evidence “hinting that ‘*A. afarensis*’ had retained some limited capacity for abducting its big toe to enhance the grasping ability of the foot” (p. 168). Perhaps the Burtele foot bones belonged to *A. afarensis*. That would explain the two different types of fossil footprints found at the Laetoli, Tanzania site.<sup>12</sup> Cartmill and Smith cite expert Russell

Tuttle, who argues that the footprints at Site G “are like those of modern humans and could not have been made by the long-toed feet of *A. afarensis*” (p. 182). The simplest explanation is that they were made by humans, as were the footprints at Site S, but that the apelike footprints from Site A were made by *A. afarensis*.<sup>13</sup> As the Laetoli footprint-bearing stratum has been dated to 3.66 Ma, no evolutionary paleoanthropologist will admit that the Site G and S footprints were made by humans, as that would collapse their human evolution storyline.

There are also questions about whether the big male KSD-VP-1/1 *A. afarensis* skeleton represents a different species (p. 172). In my opinion, the KSD-VP-1/1 *A. afarensis* skeleton likely represents *Homo erectus*, but, because of its supposed early age of 3.6 Ma, this is a possibility evolutionists cannot entertain,<sup>14</sup> for similar reasons as above.

In this chapter, and the ones that follow, the authors present contrasting views on specimens and/or species from different experts, as well as their own opinion. One suggestion is that *Kenyanthropus platyops* (figure 2) may

represent a mere variant of *A. afarensis* (p. 154). There are indications that *Australopithecus bahrelghazali* “can be encompassed within the range of variation” of *A. afarensis* (p. 153). Some experts have dismissed *Australopithecus sediba* “as just a slightly derived (and unexpectedly late) descendant or representative” of *A. africanus* (p. 160).

On this topic, in a recent paper titled “Reappraising the palaeobiology of *Australopithecus*”, paleoanthropologist Zeresenay Alemseged reduced the number of *Australopithecus* species to ‘probably’ five (i.e. *A. afarensis*, *A. africanus*, *A. garhi*, *A. platyops*, and *A. sediba*).<sup>15</sup> In the Cartmill and Smith book, the fossils attributed to *Australopithecus anamensis* are said to be the “oldest fossils that all experts acknowledge as hominin” (p. 146). Alemseged sinks *Australopithecus anamensis*, as well as *Australopithecus bahrelghazali* and *Australopithecus deyiremeda*, into *A. afarensis*. And he considers *Paranthropus* (i.e. the robust australopithecines, usually considered an evolutionary dead end) a monophyletic genus.<sup>15</sup> He thinks *Australopithecus prometheus* is best explained by intraspecific variation in *Australopithecus africanus*, and renames *Kenyanthropus platyops* to *Australopithecus platyops*.<sup>15</sup>

Hence, if you are looking for stability and certainty, it is unlikely to be found in the tale of human evolution. This is further illustrated in the comments of Bernard Wood, a doyen of evolutionary paleoanthropology, and Alexis Ulutku. In a recent *American Scientist* article, they give their opinion on popular evolutionary narratives, e.g. on supposedly

“... how, when, and why our human ancestors’ posture became upright, their gait became bipedal, their diet shifted from vegetarian to a combination of meat and plants, and their brains enlarged.”<sup>16</sup>

They state:

“Although a narrative of this type would look like an accurate account of human evolution, it would almost certainly differ from the real evolutionary history. Instead, this article will lay out reasons for thinking the existing human fossil record is incomplete in almost all respects, with little chance that any narrative explanation offered today can be the right one. If the human evolutionary story were a play or a novel, many of its characters would be absent, misrepresented, or poorly developed, and the plot would have many holes.”<sup>16</sup>

### ***Homo habilis* and *Homo erectus***

Chapter 5 is about *Homo habilis* (figure 3) and *Homo erectus*, as well as some odd fossil finds, e.g. *Homo floresiensis* and *Homo naledi*. Of interest is them mentioning that the OH 8 foot, originally assigned to *H. habilis*, is “probably of *Australopithecus boisei*” (p. 198), a robust australopithecine. Also, the type specimen of *H. habilis* (OH 7) was early on accommodated within *Australopithecus africanus* by some experts (p. 199). They mention that, apart from a bigger brain, the famous KMN ER 1470 skull “does not differ much from some [a]ustralopithecines” (p. 204). The 1470 skull is sometimes assigned to *Homo rudolfensis* when *H. habilis* is defined in a more restrictive manner. In specimens attributed to *H. habilis*, associations between craniodental and postcranial bones are rare. Where they are present (e.g. OH 62 and KMN-ER 3735), the remains are described as ‘exasperatingly incomplete’, and, if anything, their limb proportions are like *Australopithecus afarensis*, or even more apelike (p. 209).

Concerning the classification of *H. habilis*, the authors state that they “would personally prefer to retain them in a paraphyletic genus



**Figure 3.** Cast of the adult KMN-ER 1470 *Homo habilis* cranium from Koobi Fora, Kenya (discovered in 1972). Photo: Peter Line.

*Australopithecus* until more is known about their anatomy and phylogeny” (p. 214). My assessment is that *H. habilis* appears to be a phantom species, i.e. a composite species made up of mostly australopithecine remains, but also a few *Homo erectus* remains, that have been bundled together and marketed as a species of ‘apeman’. Other evolutionists have also suggested that *H. habilis* fossils should be removed from the genus *Homo*. Wood and Collard, in 1999, recommended that *H. habilis* should be transferred to *Australopithecus*, reasoning:

“*H. habilis* and *H. rudolfensis* (or *Homo habilis sensu lato* for those who do not subscribe to the taxonomic subdivision of ‘early *Homo*’) should be removed from *Homo*. The obvious taxonomic alternative, which is to transfer one or both of the taxa to one of the existing early hominin genera, is not without problems, but we recommend that, for the time being, both *H. habilis* and *H. rudolfensis* should be transferred to the genus *Australopithecus*.”<sup>17</sup>

Concerning *H. erectus*, the authors point out the different views,

with some wanting to split *Homo erectus* into multiple species, whereas others “argue that even the species *H. erectus* is one species too many, and contend that all these early humans should be formally sunk into our own species, *H. sapiens*” (p. 217). The book gives a brief history of *H. erectus*, including the find of the first specimen in Java, Indonesia in 1891, as well as the later discovery (and loss in World War II) of Peking Man in China. The authors then discuss many of the other important finds since then, including the Dmanisi specimens from Georgia, and are quite detailed in this.

Of interest is that the authors admit to assigning the Kocabas cranium from Turkey to the Heidelberg (i.e. associated with *Homo heidelbergensis*) in the first edition of the book, even though it was attributed to *H. erectus* by those who published the paper on it (p. 264). An influence in that decision was the alleged date of around 0.51 to 0.49 Ma. However, when a new date of 1.1 Ma was found, they subsequently attributed the Kocabas cranium to *H. erectus* (p. 264). Not only does this illustrate how the alleged ages of some of these fossils are fluid, but



**Figure 4.** Cast of the juvenile ADT6-69 *Homo antecessor* partial face from Grand Dolina, Atapuerca, Spain. The ADT6-15 frontal bone and ADT6-69 lower face were discovered in 1994 and 1995 respectively, and are assigned to the same individual named ADT6-69. Photo: Peter Line.

also how the assigned geological age influences species attribution. It also brings up the issue as to why *H. erectus* and *H. heidelbergensis* are classified as different species, apart from evolutionary propaganda. The authors state:

“The distinctiveness of *H. ergaster*, *H. antecessor*, *H. georgicus*, *H. gautengensis* and even *H. heidelbergensis* (see Chapter 6) from *H. erectus*, or of Heidelbergers from Neandertals, is far from unequivocally demonstrated by the pertinent fossil record. Increased knowledge may prove that some or all of these taxonomic designations are valid, but none of them are conclusively supported by currently available facts” (p. 276).

This chapter also discusses *Homo floresiensis*, better known as the hobbit, from the Indonesian island of Flores. The authors discuss three models to explain the strange fossils; the insular dwarfed *H. erectus* model, the pathological modern human model, and the pre-Erectine hominin model (i.e. they evolved from a pre-*H. erectus* ancestor) (p. 271–272). From this they state, “we incline towards interpreting it as a late survivor of a pre-Erectine

offshoot from the base of the human genus” (p. 272).

*Homo naledi* from the Rising Star cave system in South Africa is also discussed. Their view is that “the humans from Rising Star show no particular affinities to any other group of early *Homo* and that their designation as a separate species is probably justified” (p. 274). My view is that in both instances one is dealing with *H. erectus*-like individuals, with some members of the group suffering from a pathology, most likely cretinism.<sup>18,19</sup> I consider *H. erectus* individuals to have been early post-Flood humans that were robustly built,<sup>20</sup> as were the *Homo heidelbergensis* and Neanderthal individuals covered in the subsequent two chapters.

### *Homo heidelbergensis*

Chapter 6 is about supposed hominins associated with the evolutionary geological age known as the Middle Pleistocene. Hence, these fossils are often called ‘Middle Pleistocene hominins’. They are also known as *Homo heidelbergensis*—when broadly defined. The authors refer to them more loosely as Heidelbergers, and state they

“will focus mainly on specimens and sites between ca. 500 Ky and 200 Ky in age” (p. 281). A detailed coverage of the fossils is given, whether from Eurasia or Africa.

As indicated earlier, the fragility of *H. heidelbergensis* as a species is illustrated by the many specimens in it that were previously (or still are) assigned to other taxonomic groups, usually *H. erectus*. Take the Ceprano cranium from Italy. Initially dated at approximately 0.8 Ma, it was considered as the earliest European *H. erectus* (p. 296), or as belonging to *Homo antecessor* (p. 297) (figure 4). The latter is a rather shaky category also, at least according to the authors (p. 267). It was later ‘dated’ to a geological age only about half as old (p. 297), which, it was said, “pushes the specimen squarely into the Heidelberg time frame” (p. 267). As stated by the authors, “Accordingly, recent studies have emphasized Ceprano’s more derived features and sought to label it as a Heidelberg” (p. 297); i.e. as part of the *H. heidelbergensis* taxon.

The Ngandong crania from Java, Indonesia, are regarded as late-surviving *H. erectus* by many (pp. 313, 327), but are covered in this chapter on the Heidelbergers. These fossil crania are said to “present perplexing problems in terms of both taxonomy and chronology” (p. 313). Because of morphological similarities they are regarded as reflecting “regional continuity” to “earlier Javan Erectines” (p. 314). According to the authors, the “current date estimates for these archaic-looking fossils are surprisingly late, even if we group them with the Heidelbergers” (p. 314). At the end of the Heidelberg chapter, Cartmill and Smith write:

“A quick review of all the specimens described in this chapter will show that there are no unique defining characters for Heidelbergers—just various mosaics of features that are not the same for all regions, or even for all specimens within a region” (p. 330).

They further state that it “is also not clear that the species *H. heidelbergensis* has any practical utility in classification” (p. 330). Later in the book, they advance the view that most of the specimens discussed in the Heidelberg chapter, including the Ngandong remains, should be designated as a subspecies of *Homo sapiens* (pp. 467–468). In my opinion, *H. heidelbergensis* appears to have been a species name used simply to fill a supposed evolutionary taxonomic vacuum; i.e. as a transitional form between *Homo sapiens* (modern humans) and *H. erectus*, a vacuum that never existed. Like us, they were fully human, as were members of *H. erectus*. They all belong to the same species.

### Neanderthals

The focus of chapter 7 is the Neanderthals, and it is quite detailed, reflecting the abundance of material available on these specimens. A minimum of about 500 Neanderthal individuals were said to be known at the time of writing, “ranging from relatively complete skeletons to fragments of a single bone” (p. 339). The Neanderthals, especially the European ones, are said to exhibit “a strikingly cold-adapted body build”, “with short limbs, a deep wide trunk, and large body masses for their relatively short stature” (p. 368). It is said that

“... even very young Neandertals show features of skeletal anatomy and shape that distinguish them from similar modern children and foreshadow the morphology of Neandertal adults” (p. 375).

However, on whether Neanderthals and modern humans were separate species, the authors state that “If we adopt a strict biological-species definition, then the two were not separate species” (p. 407). Towards the end of the book, they opine that “Neandertals should be considered a human subspecies—*Homo sapiens neanderthalensis*” (p. 467). Also, the authors acknowledge that

“Recent reassessments of Neandertal cognition and technology ... have undermined the long-standing belief that Neandertals differed qualitatively from early moderns in cognitive capacities” (p. 406).

There is also a relatively brief section on the Denisovans in this chapter. The authors’ list of candidate Denisovans includes the Ngandong specimens from Java, as well as specimens from China, such as Dali, Xuchang, Harbin, and Jinniushan, but it is said that “none of these fossils have so far yielded macromolecules that can be used to test for Denisovan affinities” (p. 382).

### Modern humans

The last chapter is about modern humans or ‘early’ modern humans. As with the other chapters, the authors give a detailed overview of the fossil evidence. Concerning this, they state that

“... in southern and northern Africa, East Asia, Australasia, and Europe, early modern populations retained a few morphological characteristics that evidently derived from local archaic peoples” (p. 465).

They discuss several models of modern human origins, and believe the facts are best explained by the Assimilation model (p. 468). What this does indicate is that the ‘modern’ humans and robust (‘archaic’) humans did interbreed, and so had to be of the same biological species.

### Conclusion

*The Human Lineage* summarizes a lot of information and is not a light read. The authors have put a lot of effort into the book, and their knowledge in this area is considerable. However, their evolutionary worldview is incorrect, and so a lot of the discussions in the book are on information interpreted according to a false belief system, limiting its usefulness. To someone aware of this limitation, and who has a keen interest

in human origins, *The Human Lineage* can be a useful reference source on the fossils. Apart from this, I do not recommend the book.

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# David Berlinski on human uniqueness, free will, computer intelligence, and organic evolution

**Science After Babel**

David Berlinski

Discovery Institute Press, Seattle, 2023

*John Woodmorappe*

**D**avid Berlinski is described as a polymath—a term that describes a scholar who is skilled in several different fields. He holds a Ph.D. from Princeton University and has taught philosophy and mathematics at various universities in France and in the U.S. He is one of the leaders of the Intelligent Design Movement, and is a Senior Fellow of the Discovery Institute.

## Perhaps too many subjects under one book cover

This book does not appear to have a central theme. It consists of an assortment of widely-disparate topics, such as the nature of probability, the sophistication of computers, the possibilities of extraterrestrial life, the Cambrian explosion, the peppered moth, the nature and limitations of cladograms, the question of chimpanzee language, quantum mechanics, and the reality or illusion of human free will. In this respect, the fact that Berlinski is a polymath may be a two-edged sword. Some readers may find this book a disappointing series of unrelated matters thrown together.

A number of the chapters in this book involve advanced mathematics, and these can be appreciated and evaluated only by advanced and specialized readers. In this review, I bypass them and primarily focus on Berlinski's ideas on biology. Even then, I generally avoid things, verbalized by Berlinski, that have been said many times before.

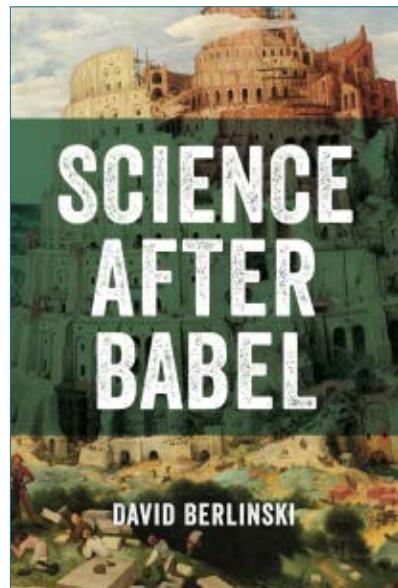
## Extraterrestrial life? We still know absolutely nothing about it

In view of the fact that there appears to be a renewed media infatuation about extraterrestrial life and extraterrestrial intelligence, the following warning by Berlinski is timely,

*“So where are they? No one knows; no one has ever detected the slightest suggestion of life beyond Earth. The Bad Thing now follows in the form of a dilemma. Either Earth is unique, after all, or life must be quite common in the cosmos. It is not common at all. Earth must, therefore, be unique. If this is so, why is it so [emphases in original]?” (p. 66)?*

## Hiding evolution's failures under a misconception about probability

The evolutionistic notion that life could spontaneously come from non-life is often glossed over by the deflection that improbable events can happen because, after all, improbable



events happen all the time. Berlinski strongly rejects this kind of thinking. He writes:

“It is worthwhile, if only as an aside, to reject the surprisingly common misconception that improbable events happen *all* the time. In time snatched from *geschaeft*, physicists often make very similar claims, especially when they are assuring one another that creationism is a form of folly. If unlikely events happened all the time, they would not be unlikely. On the contrary. Unlikely events happen as often as the laws of probability suggest. The thesis that for all times, there is *some* unlikely event that is apt to occur is trivial; and the thesis that for some unlikely event, *it* happens all the time is silly [emphases in original]” (pp. 57–58).

## The Cambrian explosion remains a glaring reality, early fauna notwithstanding

Berlinski reiterates and updates the discussion in his earlier works:

“Representatives of twenty-three of the roughly twenty-seven fossilized animal phyla, and the roughly

thirty-six animal phyla overall, are present in the Cambrian fossil record. Twenty of these twenty-three major groups make their appearance with no discernable ancestral forms in either earlier Cambrian strata or Precambrian strata. Representatives of the remaining three or so animal phyla originate in the late Precambrian, but they do so as abruptly as the animals that appeared first in the Cambrian and they lack clear affinities with the representatives of the twenty or so phyla that first appear in the Cambrian" (p. 76).

An evolutionist, Nick Matzke, has called attention to a diversity of early arthropod-like creatures in the late Precambrian. For him, these are evidence of an evolutionary radiation that culminated in the appearance of the phyla. However, by his own admission (p. 77), these early forms cannot unambiguously be related to any of the Cambrian phyla (even if one approaches the data with a prior belief in evolution). According to Berlinski, this candid admission was subsequently censored out of the Wikipedia article that bore it, but survives in other sources (p. 274).

#### **Cladistics does not prove evolution: cladistics assumes evolution**

Berlinski does not think much of the usual evolutionary methodology of making cladograms (a type of branching diagram). In fact, he uses a little sarcasm about it:

"The great merit of cladistics analysis is just the work that it makes for cladistics analysts. Like so much in Darwinian biology, it is a gift that keeps on giving. A cladistics system expresses a complicated jumble of assumptions and definitions, these expressed most often in the baroque and oddly

beautiful vocabulary of Greek and Latin technical terms" (p. 80).

More fundamentally, “‘Evolution[ary theory] is not a necessary assumption of cladistics’, the biologist A.V.Z. Brower once remarked. Neither is it sufficient, I would add” (p. 82).

I illustrated this basic fact a long time ago.<sup>1</sup> Various man-made vehicles can be arranged into a plausible clade, all having the shared derived trait of having at least one pneumatic wheel (figure 1). But no-one seriously suggests that 18-wheel trucks ultimately evolved from unicycles or that a unicycle is, cladistically speaking, an early form of an 18-wheel truck.

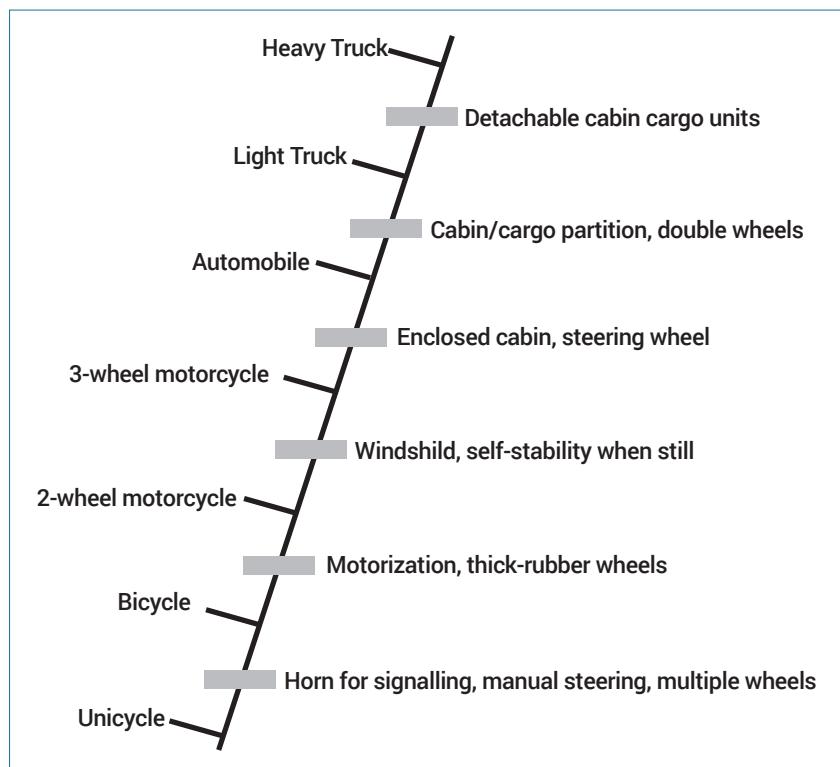
#### **Chimps and humans: exposing (the late) leading evolutionist Stephen Jay Gould**

Harvard's Stephen Jay Gould scorned Westerners for not fully

embracing evolution and chided them for stubbornly retaining the belief that there is a fundamental difference between chimps and humans. He would have had us believe that there is no distinction between the two: the difference is one of degree, not of kind. Berlinski returns the scoffing:

"No distinction? Seriously, folks? ... Chimpanzees cannot read or write; they do not paint or compose music, or do mathematics; they form no real communities, only loose-knit wandering tribes ... . There is no such thing as animal *culture*; animals do not compromise and cannot count; there is not a trace in the animal world of virtually any of the powerful and poorly understood powers and properties of the human mind ... [emphasis in original]" (pp. 89–90).

Berlinski also challenges the claim that chimps can ‘talk’ through sign language. He comments:



**Figure 1.** A cladogram can be created that has absolutely nothing to do with evolution. The shared derived trait of this spoof clade is the pneumatic wheel.

“Videotapes taken of chimpanzees revealed, when carefully analyzed, that what had passed for chimpanzee conversation was nothing more than prompted signings in the best of cases—a record of the beast’s pathetic endeavor to say whatever it was that his trainer wished him to say; in the worst of cases, the beast simply babbled (*More Me More More!*), his signs utterly devoid of meaning . . . Ever credulous, scientists now report that they have engaged the dolphin in stimulating conversations” (p. 92).

To insist that the difference between humans and chimps is one of degree, not kind, is to trivialize the very concept of degree. Berlinski compares it to saying that the difference between the Canada goose and the human, in terms of getting off the ground, is one of degree and not kind.

### Pretensions against the existence of human free will

Berlinski has no patience with those who claim that science has proven that humans have no free will. This notion centres on the *non sequitur* that, just because physics explains the behaviour of all matter, and the human being is composed of matter, all human ideas and actions are reducible to the laws of physics and are therefore predetermined. Consider the likes of Newton, Schrödinger, and especially quantum mechanics, all of which are said to leave no room for free will. He writes, “No room? Really? Quantum mechanics leaves room enough hospitably to accommodate any number of gabbling philosophers. The place is a polemical paradise” (p. 121). Berlinski unambiguously declares, “The laws of physics do nothing to prevent a man from acting freely” (p. 266).

### Computer capabilities: unlimited or limited?

Nowadays, we often encounter the fear that computer programs, including AI (artificial intelligence), will grow out of control and enslave the human race. Then we realize that so-called artificial intelligence is not true intelligence. It is a computerized usage of previously developed human problem-solving procedures. The computer does not ‘think’. It merely executes the programs that thinking humans have fed into it.

Consider another example. When we appreciate the growing accuracy of computerized language-translations, we realize that the computers are not engaging in linguistic reasoning (or any other kind of reasoning). The computer translation programs are simply comparing one language (words, phrases, and sentences; all in broader context) with a large database of previously translated words, phrases, and sentences, all in broader context. As the size and complexity of the human-made database increases, so does the ‘natural’ character of the computer-made translations.

Berlinski warns against the exaggeration of computer capabilities. He comments:

“Computers are getting faster. According to Moore’s law computer processing speed doubles every two years . . . But speed is one thing, sophistication quite another . . . sophistication has grown by roughly a linear factor . . . If computer sophistication proceeded as rapidly as computer speed, we would expect to see very sophisticated systems everywhere. This is obviously not the case . . . We do not see computers nearly as sophisticated in most cognitive tasks as a three-year-old child, or an otherwise intelligent ape, for that matter, because we do not have the requisite scientific theory to explain what they do” (pp. 65–66).

### Conclusions

Many things we are taught in popular culture about the powers of science turn out to be questionable. Computers cannot ‘think’, and physics has not proved that human free will is non-existent. Chimps and humans are not almost the same. Chimps cannot talk through sign language, and the gulf between humans and chimps remains huge. The Cambrian explosion remains very real. All in all, evolutionary theory is as flawed as ever.

### References

- Woodmorappe, J., [Walking whales, nested hierarchies, and chimeras: do they exist?](#) *J. Creation* 16(1):111–119, 2002.

# Uplifting archaeology

## **Where God Came Down: The archaeological evidence**

Joel P. Kramer

Expedition Bible, Brigham City, UT, 2020

Gavin Cox

Joel P. Kramer resides in Amman, Jordan, with his wife and three children, while serving as an adjunct professor at Shepherds Theological Seminary in Cary, North Carolina. He spent almost a decade in Jerusalem, obtaining an M.A. in archaeology from the University of the Holy Land. Under archaeologist Dr Shimon Gibson, Kramer gained practical field experience by participating in excavations in Jerusalem, Bethlehem, and Ai. Kramer is currently busy with speaking, teaching, biblical tours, archaeological research, writing projects, and maintains an informative YouTube site, *Expedition Bible*.<sup>1</sup>

### About the book

Kramer has published an attractive book, *Where God came down* (WGCD), detailing ten significant archaeological sites in Jerusalem of fundamental importance to Judaism, Christianity, and Islam. I found WGCD fascinating, revealing, and eyecatching. I learned a lot, and I consider it a must for touring Jerusalem. WGCD is not about ‘dry archaeology’; rather, it is devotional in nature (with around 95 biblical references), making it an uplifting read. Its 158 pages are endowed with 223 colour images (by Kramer and family), including drone photography of Jerusalem’s sites, photos, 3D diagrams, maps, and archive material. WGCD is a glossy hardcover book, covering 10 chapters

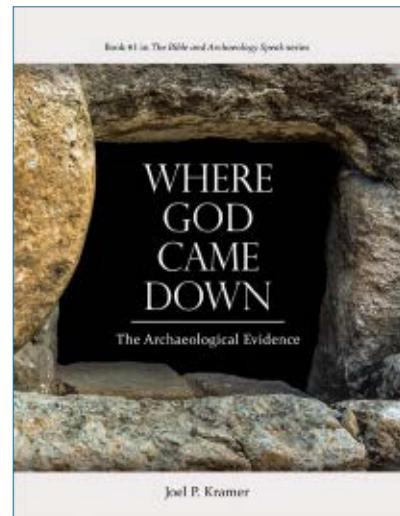
with endnotes, a conclusion, bibliography (53 citations), and a topic index (4 pages), although it lacks a Scripture index. It is a well-laid-out and attractive-looking book, but a tad expensive at US\$26.99.

Ten topics are divided into two parts, covering both Old and New Testament sites. Part 1: Abraham’s Mamre altar, Moriah’s Temple mount, Bethel, Abraham’s burial cave (Machpelah), and the City of David. Part 2 deals with five holy places: The Church of the Annunciation (where Gabriel is believed to have called Mary), Jesus’ birthplace (Bethlehem cave), Golgotha, the Garden Tomb, the Mount of Olives, and the Upper Room (Passover and Pentecost).

Kramer investigates each dig site in the Holy Land, focusing on locations where divine encounters occurred. Hence the title, WGCD. By documenting each layer of excavation, from present-day structures to older remains, Kramer establishes a compelling case for the trustworthiness of the biblical record. WGCD highlights the correlations between Scripture, archaeology, tradition, and historical texts. Kramer employs Scripture as his primary ancient text and interpretive tool, analyzing the archaeological record behind the ten locations.<sup>2</sup>

### Introductory thoughts ...

Kramer cites archaeologist Dr Amnon Ben-Tor to good effect, “Eliminate the Bible from the archaeology of the Land of Israel ... and you have deprived it of its soul” (p. 7). Stones cannot speak for themselves. Kramer explains, using the illustration of the box-lid of a puzzle, how Scripture presents the ‘big picture’. This is how biblical archaeology relates to the Bible; only one percent survives (akin to a



handful of surviving puzzle pieces), but, for those who will allow it, the Bible provides the big picture. Archaeologists excavating in Israel are predominantly doing so from a secular viewpoint, so their interpretation of evidence, rather than the data itself, may lead them to contradict (rather than uphold) the Bible’s account of history (p. 8).

### Abraham’s altar at Mamre

The first chapter lays down the groundwork for the rest of his book. Multiple layers of stratigraphy, and historical texts, all point back to specific, significant origins. Kramer discusses the excavations of Mamre, where Abraham raised an altar after receiving the promise of a son (Genesis 18). Two archaeologists have excavated Mamre, the German Evaristus Mader (1926–1928), and Yitzhak Magden (1984–1986). It consists of five layers of structures all built over the other, leading down to bedrock. Here, conspicuous holes, caused by tree roots (possibly Mamre’s oak trees), were uncovered beside a well. The bedrock was marked by consecutive structures; right into the Islamic period (begun in AD 638). Firstly, an Iron Age Israelite gated walled enclosure and altar (dated by pottery to 1000–586 BC), marked the



**Figure 1.** Model of Herod's Second Temple

site. Later, Herod built large enclosing walls, surrounding the Iron Age altar. Later still, Greeks observed the site as holy, by sacrificing to Hermes. Then around AD 324, a textual confirmation by Constantine confirms that this was the site of Abraham's Mamre altar. Constantine built a church on the site, thereby extinguishing the Greek pagan worship. Kramer points out that Constantine built only four churches in the Holy Land, one at Mamre, signifying its importance for Christendom.

“What makes the site of Mamre profound? The Lord stood there and conversed with Abraham. Mamre is holy ground” (p. 15).

Here at Mamre, God promised He would make Abraham into a mighty nation, thereby blessing all nations (Genesis 18:1, 18). This site is therefore one of the most sacred in Judaism. Many Christians believe that the pre-incarnate Christ appeared to Abraham, giving him the promise. Kramer points out, “Jesus gave the promise. Jesus was the promise” (p. 22).

Finally, after Muslims had conquered Jerusalem (AD 638), a further construction commemorated the altar made by Abraham, who is revered in Islam as a prophet.

Kramer makes the point that such examples of discovery through

archaeology refute the biblical minimalists. For instance, Israel Finkelstein has gone into print with statements casting a slur on the biblical record. Archaeological discoveries in Israel have, in Finkelstein’s opinion:

“... cast serious doubt on the historical basis of such famous biblical stories as the wanderings of the patriarchs ... Some of the most famous events in the Bible clearly never happened at all” (p. 21).

This is why biblical archaeology is imperative—to counter rank disbelief.

Kramer summarizes his impressions of this first archaeological site by explaining that the promise to Abraham was fulfilled and the archaeological stratigraphy corroborates this fact. Layer 1: Abraham received the promise of a son, Isaac, from whom would come the people of Israel. Layer 2 commemorates the kingdom of Israel. From the line of those kings was born Herod the Great. He tried to kill the promised child, all the while building protective walls around the altar (ironically, to the promised son), marked by layer 3. Layer 4 testifies to the fact that, through the promised son, the whole earth was blessed. This is demonstrated in the construction made in the Christian era, under the (so claimed) Christian Roman emperor Constantine. Kramer concludes:

“... cast serious doubt on the historical basis of such famous biblical stories as the wanderings of the patriarchs ... Some of the most famous events in the Bible clearly never happened at all” (p. 21).

“Mamre has been, and still is, a place to remember and worship the One promising and the One promised—Jesus, son of Abraham, Son of God, blessing to all the world” (p. 23).

### Moriah—the Mountain of God

Mount Moriah marks the event of Abraham’s greatest test, the sacrifice of his promised son. It also marks the greatest revelation of redemption, in the form of the promised Lamb (Genesis 22). However, Mount Moriah has never been excavated, being the site of Islam’s Dome of the Rock, and Israel’s Temple Mount, making it a highly sensitive area. Therefore, a complete picture of archaeology can only be pieced together from scriptural evidence, historical texts, and visible archaeological features.

The next episode in the development of the Temple Mount area was the purchase of the threshing floor of Araunah by King David (II Samuel 24:15, 16–19, 24–25). This was a good lesson for me as, in my mind, I had not linked this episode with Abraham’s Moriah and the Temple. At II Chronicles 3:1, the link is established. Here, Solomon began to build the Temple on Mount Moriah on the location of David’s threshing floor. The Holy of Holies likely sat directly over David’s (and Abraham’s) altar. Tragically, in 586 BC, King Nebuchadnezzar of Babylon destroyed Solomon’s Temple (II Kings 25:9). 70 years later, Zerubbabel erected the new temple on the same site (Ezra 6:3, 7).

The next layer of construction was King Herod’s Second Temple in the first century BC. The Jewish historian Josephus described its magnificence (figure 1).

Jesus prophesied its destruction with very specific words—that “not one single stone will be left that will not be thrown down” (Matt 24:1–2). Jesus’ words were fulfilled in AD 70, when Vespasian’s son Titus destroyed Jerusalem. His words were vividly

brought to life by the excavations of Israeli archaeologist Benjamin Mazar (1968–1982), who uncovered huge stones at the base of the Temple Mount platform. I once visited this site during a tour of Old Jerusalem and was moved at the site of the block pile, which had smashed the underlying pavement.

In AD 130, Roman emperor Hadrian built a pagan shrine to Jupiter and Hermes on the site, which, according to Church Father Jerome, existed into the 4<sup>th</sup> century. During the Byzantine period (AD 324–638), Hadrian's shrine was demolished, and the site lay barren, until the Islamic conquest. I was interested to read of the account of the invading Muslim Caliph Omar, who negotiated for the Mount with Sophronius, the Byzantine bishop of Jerusalem. Sophronius stated that the Christians had not built a church on Moriah in respect of Jesus' prophecy (Matt 24:1–2). A later caliph, Abd al-Malik, built the Dome of the Rock over the rocky outcrop of Moriah. The rocky peak, exposed within the mosque, is still visible (figures 2, 3).

Kramer reviews all eight stages of Mount Moriah's development to the present day. Clearly, the archaeology and textual evidence point to this as being the place of Abraham's sacrificial altar and the Holy of Holies of Israel's temple.

The third site that Herod enclosed with walls is Abraham's burial cave at Machpelah (Genesis 49:30). Kramer discusses this site more briefly, stopping at the Herodian period. However, there is a much later, notable, history to this site, involving various building and restoration works. Thus, a witness is established to the importance of the site in the eyes of Jews, Christians, and Muslims. It is currently under Muslim administration, so, sadly, archaeological investigation is prohibited.

### Kramer the creationist

Kramer defends the historicity of the Genesis creation account, and



Image: Library of Congress, Wikimedia / PD



Image: Berthold Werner, Wikimedia / PD

**Figure 2.** Moriah's 'Foundation Stone' in the floor of the Dome of the Rock, Jerusalem

maintains that Genesis forms the bedrock to the Gospels:

"The Bible tells us about two gardens: the Garden of Eden and a garden in Jerusalem. Eden's garden held perfection and newly-created life . . . These two gardens are the stages upon which the critical plot line of the story of mankind's relationship with God played out. In the first garden, man disobeyed, sin entered, death came, and God's relationship with mankind was broken. In the second garden, the Son of Man obeyed, sin was paid for, death was destroyed, and a way for relationship with God restored" (p. 111, cf. p. 120).

These are profound statements and are to be commended.<sup>3</sup>

### Conclusion

Kramer asks us to accept each site as the 'legitimate' site for each biblical location. Unfortunately, there are no discussions of (the many) alternate sites, which is the major weakness of his book. For instance, no discussion is offered for the traditional Garden Tomb, or Golgotha's 'Place of the Skull', which seem to be glaring omissions. When I used to consider the possible location of the New Testament sites, I was inclined to

think, 'does it really matter'? From the preponderance of evidence discussed in WGCD, readers will be provoked into seeing that there is more to consider here than mere quaint 'tradition'. As Kramer concludes, "For some, examining the evidence found in those places will play a role in their coming to believe" (p. 147). That, to me, is the essential reason—that people recognize the Bible is trustworthy, and so trust the Saviour. It is for this reason I happily recommend Kramer's book.

### References

1. Kramer's many videos of biblical archaeology can be viewed at [youtube.com/@ExpeditionBible](https://youtube.com/@ExpeditionBible).
2. Kramer has a helpful webpage that has information about him and some useful bonus material in the form of four videos explaining various sites: Bethlehem, the Mountain of the Lord, Jerusalem's topography, the Bible as an archaeological tool, [wherегодcamedown.com](https://wherегодcamedown.com), accessed 18 May 2023.
3. For instance, Shepherds Theological Seminary require their staff to sign up to their statement of faith, which includes an adherence to 6-day special creation as a historic event, as described in Genesis 1–2, [Shepherds Theological Seminary doctrinal statement](https://shepherds.org/doctrinal-statement), accessed 23 May 2023.

# Who wrote Genesis?—the internal evidence

David Malcolm

There are various views on who wrote the source documents Moses used to write the book of Genesis. These are discussed here. One (minority) view is that Genesis contains wording indicating who the actual authors were; in most cases, authors who were close to the events they record. This paper supports this minority view.

We can assume that Moses was the author of the first five books of the Bible (the Pentateuch). The documentary hypothesis lacks any historical evidence. We have five whole books telling us in great detail about Moses' life and his interaction with God. If Moses was not the author of those five books, they would have no legitimacy whatsoever. Any further discussion on that matter seems unnecessary.

But the question arises: where did Moses get his information for the book of Genesis? He tells us about events well before his time, some thousands of years before. The idea that oral accounts passed down over the generations strains credulity. Who could remember all those numbers? Along with most creationists, I am convinced by the evidence that Moses used pre-existing written records. However opinions differ between creationists as to exactly how those written records came to Moses, and who the authors were. The main issue is the understanding of the *toledoth* passages (see shortly).

However, opinions differ between creationists as to exactly how those original written records came to Moses. This presentation will promote what is the minority view. The reader's attention will be drawn to the many lines of evidence internal to the book of Genesis itself. However, this presentation should also be seen as a continuation of the dialogue looking at the question of the actual authorship of the source documents. We all come with biases, and the biased position of the present author is that we are told who the authors were; an opinion formed from reading Dr C.V. Taylor's book *The Oldest (Science) Book in the World* (figure 1).<sup>1</sup> To those readers who come with a different perspective, it is to be hoped they will give this material careful consideration rather than rejecting it outright.

## The *toledoth* passages

There are several places in Genesis where the Hebrew word *toledoth* occurs. This word is usually translated ‘generations’. On 10 occasions we read “these are the generations of”, and on another occasion the wording is “this is the book of the generations of Adam”. The verses are specifically 2:4, 5:1, 6:9, 10:1, 11:10, 11:27, 25:12, 25:19,

36:1, 36:9, and 37:2. A typical instance is “These are the generations of Noah” (Gen 6:9 RSV; figure 2). The experts seem to agree that these 11 verses mark major breaks, but there is a difference of opinion over how they should be understood. The majority view says they are an introduction to what follows, while the alternate view maintains that they mostly refer to what has gone before.

The main authority to be used for the majority view will be *The Genesis Account*, by Dr J.D. Sarfati.<sup>2</sup> And for the alternate view, that they refer to what has gone before, like a ‘sign-off’ or finishing touch at the end of a document (colophon):

- *New Discoveries in Babylonia About Genesis*, by P.J. Wiseman<sup>3</sup>
- *The Oldest (Science) Book in the World*, by Dr C.V. Taylor<sup>1</sup>
- *Who Wrote Genesis?—Are the toledoth colophons?* by Dr C.V. Taylor.<sup>4</sup>

There is no doubt that the majority opinion is that the *toledoth* passages point forward.

“Professor Ryle informs us that the use of the phrase ‘represents, as it were, successive stages in the progress of the narrative’. Commentators of all schools of thought, such as Spurrel, Lenormant, Skinner, Carpenter, Harford-Battersby, Bullinger, Lange, Keil and Wright divide the book into sections which begin with the phrase.”<sup>5</sup>

## How to decide

How do we decide what is the truth on any specific issue?

- We might go with the majority view, perhaps as we have been taught. This is generally the easiest as it avoids conflict.
- We might choose to adopt a minority view. We might take this side because we like to be different, or we may become self-satisfied because we have this extra knowledge.
- What the creationist movement seems to have adopted is to look carefully at the actual evidence; and try to evaluate it with an open mind, without being swayed by tradition or rhetoric, and while giving full weight to the biblical text.

## Arguments for the majority view

Evidence for the majority view<sup>6</sup> may be understood as follows:

1. *Toledoth* is a form of the verb<sup>7</sup> *yalad*, which means ‘the generation of posterity’,<sup>8</sup> so clearly refers forward.
2. *Toledoth* is in the hiphil verbal form, which might reinforce the idea that it refers forward.<sup>9</sup>
3. The first occurrence (Gen 2:4) clearly refers to what follows.<sup>8</sup>
4. When we read the wording ‘these are’, it invariably refers to what follows.<sup>8</sup> This is supported by passages such as Numbers 3:1, Ruth 4:18, and I Chronicles 1:29.<sup>8</sup>
5. Furthermore, the word *yalad* embodies the thought of what the progeny did in their lifetime.<sup>8</sup>

Let’s look at these arguments in detail.

*Point number 4* takes the view that ‘these are’ consistently refers forward in the book of Genesis. This is simply not the case. There are instances where ‘these are’ clearly points backwards. These verses in Genesis 10 clearly point backwards:

- These are the sons of Japheth (v. 5),
- These are the sons of Ham (v. 20),
- These are the sons of Shem (v. 31), and, in overview,
- These are the sons of Noah (v. 32).

A full analysis of the usage of ‘this’ and ‘these’ has been given by Taylor,<sup>10</sup> and is summarized in this table (excluding the instances under consideration):

Word	Passage	Anaphoric refers backwards	Cataphoric refers forwards	Exophoric refers outside
this	Genesis 1–36	68	5	12
	Genesis 37–50	32	7	5
these	Genesis 1–36	49	18	4
	Genesis 37–50	17	2	3

Even in Moses’ later writings we see the usage of backward references:

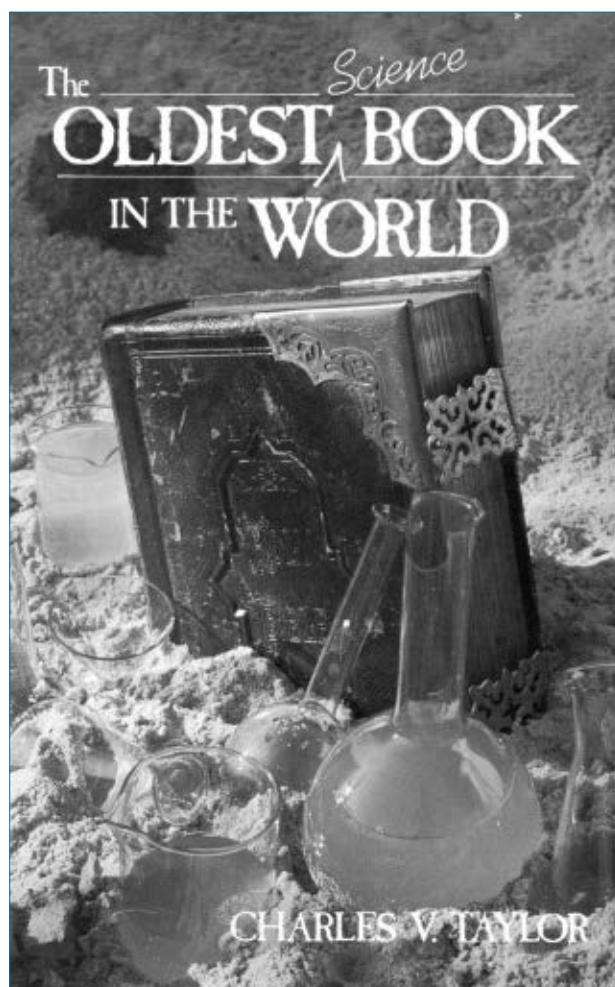
- The book of Leviticus is summarized in the last verse: “These are the commandments which the Lord commanded Moses for the children of Israel on Mount Sinai” (Leviticus 25:34 NKJV).<sup>11</sup>
- The book of Numbers is also summarized: “These are the commandments and the judgements which the Lord commanded the children of Israel by the hand of Moses in the plains of Moab by the Jordan, across from Jericho” (Numbers 36:13 NKJV).<sup>11</sup>

*Point number 2* tells us that *toledoth* is in a hiphil form of the verb (causative), which reinforces that it is a forward reference. Using Hebrew verbs in the hiphil form changes the meaning for some verbs. This table shows how the word is translated in the AV, according to Young’s Concordance:

Verb <i>yalad</i> in Genesis	Translated ‘bear’	Translated ‘beget’
Simple (qal)	68 times e.g. Gen 4:1,2	8 times e.g. Gen 10:8,13,15
Causative (hiphil)	None	40 times e.g. Gen 5:3,4,6,7

It seems that *yalad* as a qal is generally used for the mother’s part and is translated ‘bear’, while as a hiphil it is used for the father’s contribution and is translated ‘beget’, which makes sense. Beyond this there appears to be no difference in the verbal form used.

As for *point number 5*, Keil and Delitzsch are quoted as saying that *yalad* includes “the development of these generations or of his descendants; in other words, the history of those begotten or the account of what happened to them and what they performed.”<sup>8</sup> But surely to extend the meaning to include a history of the progeny is wishful thinking at



**Figure 1.** Creationist book by Dr Taylor, published in 1984 in Queensland, Australia. The book addressed a range of issues.

**אֵלֶּה תּוֹلְדָת נֹم נֶם אִישׁ צָנִיק פָּמִים גַּיה בְּלֹרְמִיו אֲתִ-הָאֱלֹהִים הַתְּהִלְדָּנִם:**

Figure 2. Genesis 6:9 in Hebrew. The first three Hebrew words (bold; read right to left) can be translated as “These are the generations of Noah”.

best. Surely they have sneaked in the conclusion they want to come to, as part of the intrinsic meaning of the verb. Is this then a classic example of circular reasoning? It could be an example of spurious arguments coming to be accepted to enhance the majority view.

With *point number 3*, experts may be quoted in support, but other experts can be quoted to refute it.

“German liberal scholars of the 19<sup>th</sup> century, as well as the English Spurrell, and Carpenter and Hartford-Battersby, wanted to move Genesis 2:4a from its place to before Genesis 1:1, because it seemed a better title to Genesis 1:1 to 2:3. ... When James Moffat produced his translation of the Bible he actually put 2:4a before 1:1, because it seemed more appropriate there.”<sup>12</sup>

It might also be significant that the AV translation has “the generations of the heavens and earth *when* they were created”, not *after* they were created.

This leaves us only with *point number 1*. Obviously, the verb of producing offspring points forward. Does that imply that we cannot talk about generations (*toledoth*) retrospectively? We talk about four-generation pictures. In figure 3, are we to believe that the only person who could call that a four-generation picture is the great-grandmother?

Taylor quotes the creationist E.J. Young, who “points to the fact that *toledoth* is derived from the verb *yalad*, ‘beget’, hence it must refer to something following or begotten by the person whose *toledoth* is being set forth. However, this sort of argument is linguistically unsound.”<sup>13</sup> He goes on to say, “Clearly the use of *toledoth* in Hebrew is not restricted to things begotten and their effect on the future. It normally refers to how one came to be begotten, as it were.”<sup>13</sup> Taylor’s opinion must carry some weight, since his special field was linguistics and ancient history.<sup>14</sup>

Wiseman quotes a Hebrew scholar to show that *toledoth* should be translated as ‘history’: “Gesenius ... explains its meaning as ‘History, especially family history, since the earliest history among oriental nations is mostly drawn from genealogical registers of families.’<sup>15</sup> Conclusive scriptural evidence is found in Numbers 1:18, where “they recited their ancestry by families, by their fathers’ houses” (NKJV). The word translated ‘ancestry’ here and ‘pedigree’ in the AV is the Hebrew word *yalad*.

Nor are instances restricted to the Old Testament:

“Even in the New Testament, we find the expression in the King James Version, ‘The book of the generation of Jesus Christ’ (Matthew 1:1), where ‘generation’ is a translation of the Greek *geneseos*, a genitive equivalent

of the Hebrew *toledoth* [emphases in original].”<sup>16</sup>

And there is one point that is highly embarrassing for the view that these passages indicate a flow forwards. The most important person in the whole book of Genesis would have to be Abraham. In Abraham, God commences his plan of redemption. From Abraham will come Israel, God’s chosen and holy people, through whom will come the saviour of mankind. The most significant verse in Genesis would therefore be “These are the generations of Abraham”. But that verse does not exist. Taylor also makes this point: “The problem here is that Terah is included and not Abraham. Are we to say Abraham was not of sufficient importance to warrant a break in the genealogies?”<sup>13</sup>

### Support for the alternate view

The alternate view may have existed as a minority view for a long time, but it was given new impetus by the writings of Wiseman from 1936, because of his insistence that colophons were the norm in ancient writings. Some writers accepted his idea of colophons in Genesis, or at least thought the idea was quite possible:

- 1936, New Discoveries in Babylonia About Genesis, by Wiseman<sup>2</sup>
- 1948, Creation Revealed in Six Days by Wiseman<sup>17</sup>
- 1969, Introduction to the Old Testament by Harrison<sup>18</sup>
- 1976, The Genesis Record by Morris<sup>19</sup>
- 1984, The Oldest (Science) Book in the World, by Taylor<sup>3</sup>
- 1994, Who Wrote Genesis? – Are the *Toledoth* Colophons? by Taylor<sup>4</sup>
- 1998, Who Wrote Genesis? Did Moses really write Genesis? by Grigg.<sup>20</sup>

Taylor argued that the *toledoth* passages are colophons:

“This insight is due to the work of Wiseman, and though I disagree with Wiseman’s theory about the six days of creation, I accept his scholarship in relation to ancient customs in what we now call Iraq and what the Greeks in classical times called Mesopotamia.”<sup>21</sup>

### Nine sections

Taylor figured that Genesis was divided into nine sections, each written by a different author(s). He made this division into nine volumes on the basis of (eight of) the *toledoth* passages. “If my theory of origins is right, then Genesis consisted originally of nine volumes as follows”:<sup>22</sup>

Vol.	Genesis Ref.	Toledoth	Contents
1	1:1–2:4a	God's book	Heavens & Earth
2	2:4b–5:2	The book of the generations of Adam	Garden of Eden Cain & Abel Birth of Seth
3	5:3–6:9a	Noah	Noah's ancestors Nephilim
4	6:9b–10:1	The sons of Noah: Shem, Ham, Japheth	Account of the Flood Rainbow Curse on Canaan
5	10:2–11:10a	Shem	Table of nations Tower of Babel
6	11:10b–11:27a	Terah	Terah's family tree
7	11:27b–25:19a	Isaac & Ishmael	Isaac's biography of Abraham with Ishmael's family tree as appendix
8	25:19b–37:2a	Esau & Jacob	Jacob's biography of Isaac & his descendants, incl. Jacob's autobio-graphy with Esau's family tree as two appendixes
9	37:2b–50:26	<i>No author stated</i>	Joseph and his brothers

According to the archaeological evidence, there was often more information associated with the colophon:

“The colophon, which concluded the individual tablet or series, normally contained the name of the scribe or the owner of the tablet ... and frequently it also included some attempt at dating. In addition, it often embodied the title given to the narrative, and if the tablet was part of a series it furnished the serial number and a statement as to whether the tablet did or did not conclude the series.”<sup>23</sup>

And these features are evident in the manuscripts of Genesis. If this is a correct definition of a colophon, then the concluding verses of Leviticus and Numbers (as previously quoted) are colophons.

If we assume that each volume was written by the person named in the colophon, we find that all the details they record are things they would have known in their lifetime.<sup>24</sup>

Volume 2—This section tells us about Adam's descendants up to Jabal, Jubal, and Tubal-Cain. “These men were the

eighth generation from Adam, and a comparison with the genealogy given in chapter 5 shows that this generation lived immediately before Adam's death”.

Volume 4—We know that Shem survived Noah by 150 years, “Hence there is nothing in this section that the sons of Noah could not have written.”

Volume 5—“Shem writes about the birth and the formation into clans of the fifth generation after him. We know that he outlived the last generation recorded in this tablet, i.e. the sons of Joktan”.

Volume 6—Terah lived until Nahor's son Abraham was 75 years old.

“Had Terah lived another 11 years he would have been able to record the birth of Ishmael, and if for another 25 years it would have been possible for him to add, ‘and Abraham begat Isaac’. But the history contained in this tablet ends immediately before his own death. If the words found at the end, ‘and Terah lived 70 years’ refer to the date he wrote it, then according to the Samaritan version it was written just one year after the last chronological event mentioned in it—the death of Nahor.”

Volume 3—Noah's genealogical list, ending with the birth of his three sons. “In this instance he could have written the story of the Flood. But this is contained in the tablets of the ‘history of the sons of Noah’.”

So we find remarkable confirmations:<sup>25</sup>

1. In no instance is an event recorded which the person or persons named could not have written from his own intimate knowledge or have obtained absolutely reliable information.
2. It is most significant that the history recorded in the sections outlined above ceases in all instances before the death of the person named, yet in most cases it is continued almost up to the date of death, or the date on which it is stated that the tablets were written.

If we allow that the date at which a section was written is recorded in some instances, then the close of Jacob's section is remarkable.

Immediately before the ending formula “These are the origins of Jacob”, we read, “and Jacob dwelt in the land of his father's sojourning, in the land of Canaan”. This sentence has seemed so isolated that it has been regarded by many to have little relation to the context, yet it is evidence of the date when and place where the tablets were written. Within a few years Jacob had moved down to Egypt, but this sentence indicates where he was living when he closed his record, for although he tells us of the death of Isaac, he says nothing whatever of the sale of Joseph into slavery, which occurred 11 years before Isaac's death. Neither does he tell of Joseph's interpretation of the butler's dream or of any other event in Egypt. Until Jacob went down to Egypt (ten years after he had buried his father), thus leaving “the land of his father's



**Figure 3.** A four-generations picture: A young boy, his mother, his grandmother (right), and his great-grandmother (centre). A photo of people spanning four generations is fairly rare.

sojourning”, he could not know anything whatever about these things. Thus, the record of Jacob closes precisely at the period indicated in the sentence in Gen 37:1.<sup>26</sup>

He had gone back to the South Country, Hebron (where his father lived), only ten years before Isaac had died, and he records his death. And within 10 years of this latter event, Jacob was himself living in Egypt. So, this hitherto obscure verse in chapter 37 clearly indicates not only that Jacob wrote the tablets, but when and where they were written.<sup>27</sup>

It cannot be a mere coincidence that each of these sections should contain only that which the person named at the end of them could have written from personal knowledge. Anyone writing even a century after these Patriarchs could and would never have written thus.<sup>27</sup>

Jean Astruc<sup>28</sup> insisted that there were three authors of the Flood account:<sup>29</sup>

Author A	The waters prevailed and were increased greatly upon the earth (7:18)	All flesh died that moved upon the face of the earth (7:21)
Author B	The waters prevailed exceedingly upon the earth (7:19)	All in whose nostrils was the breath of life and all that was in the dry land died (7:22)
Author C	Fifteen cubits upward did the waters prevail (7:20)	Every living substance was destroyed (7:23)

This would hardly be surprising if the colophon idea is correct: Shem, Ham, and Japheth were all involved in producing the account of the Flood (vol. 4 in Taylor’s list). It is only a problem if the account is due to Noah. Perhaps Shem, Ham, and Japheth each wrote their own account, then combined them.

The material given above is mainly the work of Wiseman. His paper contains a lot more interesting ideas, and so the reader is referred to that work. For example:

- Babylonian words in early chapters replaced by Egyptian words in later chapters<sup>30</sup>
- use of ‘catch lines’ to assist with arranging tablets in the correct order,<sup>31</sup> which is also evident in Genesis.

However, note that Bible believers will take issue with some of his material: specifically, he uses the timeframe accepted by the archaeological community.

### Odd features explained

There are a number of features of the text of early Genesis that leave us with questions.

“The waters prevailed fifteen cubits upward, and the mountains were covered” (Gen 7:20 NKJV). Why is 15 cubits mentioned? One commentary has this answer:

“P describes a depth of water of 15 cubits (=22 ft) above the mountains. Why should 15 cubits be mentioned? Very possibly, because the height of the ark was 30 cubits (Gen 6:15), and the ark was considered to be submerged for half its depth” (Cambridge Bible for Schools and Colleges).

Other commentaries have other explanations.

Fifteen cubits is not a lot of water compared to the height of the highest mountains. Why is this mentioned? Consider a hypothetical scenario: just suppose that Shem had worked out the principle of flotation and had figured that the Ark would float half submerged when fully loaded. Further suppose he had told all his family of his calculations and they were all somewhat concerned. Would the Ark run aground and sink? So Noah took it to the Lord, who assured him there would be at least 15 cubits of water (half the height of the Ark). That turned out to be the case, and everybody was much relieved. Then it may not even occur to the human author(s) to give any explanation. The entire world population (of eight people) understood perfectly. While this account is pure conjecture, it could be something like the reality. If anybody other than the people involved wrote this, we would expect them to give an explanation or else omit this information.

Similar considerations may apply to when Eve mistakenly supposed she was giving birth to God incarnate (Genesis 4:1), a passage that translators have difficulty with.<sup>32</sup> Eve simply made a mistake of timing. The woman giving birth to the seed (Genesis 3:15) was not to be until many generations into the future. But why are we not told that Eve made a

mistake? It was so obvious to those involved; it just didn't occur to the author that there would be readers coming later who didn't understand.

These two difficulties are resolved if we take the text as having been written by the people involved rather than as the result of a divine revelation.

We are presented with what looks like a contradiction: "Noah found grace in the eyes of the Lord" (Gen 6:8) as against "Noah was a righteous man" (Gen 6:9). But if the scheme we are suggesting is right, verse nine was part of the account by Noah's sons, who, as good sons, were honouring their father, while verse eight, by Noah himself, acknowledges his true situation before God. So the difficulty is resolved.

### Moses' contribution

It is not clear what Moses had to change to fashion the foundational book of the Bible out of the pre-existing written records. Possibly the transitions from one author to the next were added by Moses, or perhaps they were written by the original authors.

Taylor looks into the possibility that Moses may have changed words for 'God'. However, his reasoning is mixed up with the idea that somebody had to translate from the original language into Hebrew. Sarfati makes a convincing case that the original language<sup>33</sup> was Hebrew. So it is not clear whether Taylor's idea applies.

Moses may have deleted things which were not appropriate (and we wouldn't know), but, if he had very little input, that might suggest that Moses had very great respect for the ancient writings and tried to change things as little as possible.

Somebody (and it had to be Moses) has updated place names:<sup>34</sup>

Updated place name	Genesis ref.
Bela (which is Zoar)	14:2 and 8
Vale of Siddim (which is the Salt Sea)	14:3
En-Mishpat (which is Kadesh)	14:7
Valley of Shaveh (which is the King's Dale)	14:17
Ephrath (which is Bethlehem)	35:19

In these instances, he has been careful to preserve the original names together with the current names at his point in history.

In other instances, Moses has made no change to the text he inherited. Possibly the most significant of these is Genesis 10:19, "And the territory of the Canaanites extends from

Sidon, in the direction of Gerar, as far as Gaza, and in the direction of Sodom, Gomorrah, Adma and Zeboim, as far as Lasha" (RSV). Clearly Sodom and Gomorrah still existed at the time this section was written. Volume 5 was written by Shem, and these cities were not destroyed until the times of Abraham. Such instances show the historical authenticity of the texts we read.

### Conclusion

Taylor addressed the issues that have been used to promote the traditional majority view. We might conclude that he showed them to be without justification. At least it has to be agreed that he made them look highly questionable. So, although Taylor's contribution predates Sarfati's book, it should be seen as a critique of Sarfati's authorities.

Archaeological evidence has been presented by Wiseman to indicate that the colophon was normal in the most ancient of known writings. Those of us without archaeological expertise cannot evaluate his finding. Nevertheless, everybody can see that the evidence internal to the book of Genesis overwhelmingly confirms Wiseman's belief.

Thus, we can agree with Taylor and Wiseman and come to the conclusion:

"The book of Genesis was written on tablets in the ancient script of the time, by the Patriarchs who were intimately concerned with the events they related, and whose names are clearly stated. Moreover, Moses, the compiler and editor of the book, as we now have it, plainly directs attention to the source of his information."<sup>35</sup>

Thus, the true structure of Genesis consisted of the nine volumes identified by Taylor:

1. Unlike the rest of Genesis, which was written by men, volume 1 is an utterly reliable revelation from God. He revealed things we could never find out, such as the six literal days of creation in which God set up the seven-day week for our benefit. God set the literary pattern of the colophon.
2. Adam gave a true 'generations' account via his son Cain. But Adam added much more than a simple genealogy, including his eyewitness account of the beginning of things. Adam gives the all important truth about the entry of sin into the world. He concludes with the colophon, "This is the book of the generations of Adam", making it clear that it was written down. The original justification for the documentary hypothesis was the different names for God, suggesting different authorship of volumes 1 and 2. With the scheme proposed here, it is clear that they had different authors.
3. Noah gave a 'generations' account from Adam to himself. He took baked clay tablets on the Ark. Clay tablets were the preferred writing medium during the earliest period of

- human history that has been unearthed. Baked clay tablets would have been very easy to duplicate and would have been an ideal medium for Noah to have had on board the Ark at a time when there was water everywhere.
4. Observer-relative account of the Flood by Shem, Ham, and Japheth.
  5. Shem's account of history. He tells about the tower of Babel. The colophon was normal up to this time and beyond in the region near to Babel, although not elsewhere.
  6. Terah set down a 'generations' account from Noah to his day.
  7. Isaac's contribution. Colophon not used for Ishmael's account. Rather the *toledoth* verse, at Gen 25:12, is a title for the appendix that follows.
  8. Jacob's contribution. Again, a colophon is not used for either appendix. The *toledoth* verses Gen 36:1 and 9 are titles, reflecting later practice.
  9. Last section about Joseph and his brothers is of unknown authorship.

The Ancient Jewish experts (Masoretes) introduced the chapter divisions into the sacred text, and for Genesis they failed to understand the structure as now revealed. Nevertheless, credit is due to all the Jewish authorities who copied the sacred text diligently, preserving the all-important indicators.

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5. Wiseman, ref. 3, p. 45.
6. Sarfati, ref. 2, pp. 19–22.
7. In English it is customary to use the infinitive of a verb for simplicity, but for Hebrew it is normal to list the 3<sup>rd</sup> person singular past tense, as that form is simpler. Thus, *holid* and *yalad* are the same verb.
8. Sarfati, ref. 2, p. 20, quoting Keil and Delitzsch.
9. Sarfati, ref. 2, p. 21, quoting DeRouchie.
10. Taylor, ref. 4, p. 210.
11. Wiseman, ref. 3, p. 51.
12. Taylor, ref. 4, p. 208.
13. Taylor, ref. 4, p. 207.
14. Taylor, ref. 1, p. 7.
15. Wiseman, ref. 3, p. 47.
16. Taylor, ref. 4, p. 206.
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18. Harrison. Quoted by Sarfati, ref. 2, p. 19.
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20. Grigg, R., *Who wrote Genesis? Did Moses really write Genesis?* *Creation* 20(4):43–46, 1998.
21. Taylor, ref. 1, p. 21.
22. Taylor, ref. 1, p. 20.
23. Sarfati, ref. 2, p. 19, quoting Harrison, R.K., *Introduction to the Old Testament*, Eerdmans, Grand Rapids, MI, p. 545, 1969.
24. Wiseman, ref. 3, p. 55.
25. Wiseman, ref. 3, pp. 53–54.
26. Wiseman, ref. 3, pp. 56–57.
27. Wiseman, ref. 3, p. 57.
28. See information about Astruc, supplied in Sarfati, ref. 2, p. 17.
29. Wiseman, ref. 3, p. 75.
30. Wiseman, ref. 3, pp. 58–59.
31. Wiseman, ref. 3, p. 44.
32. Sarfati explains this well. See Sarfati, ref. 2, pp. 407–408.
33. Sarfati, ref. 2, p. 406, ff.
34. Wiseman, ref. 3, p. 60.
35. Wiseman, ref. 3, p. 10.

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# Blood clots in bones of dinosaurs and Permian tetrapods—evidence of asphyxiation?

Mark Armitage

Blood clots occluding microvascular bone canals have been reported in Cretaceous dinosaur remains, including those of separate individuals of *Triceratops* and *Nanotyrannus*,<sup>1–3</sup> and in *Dimetrodon*, an early Permian synapsid.<sup>4</sup> We report here newly discovered blood clots in *Edmontosaurus* (a Cretaceous hadrosaur), *Camarasaurus* (a Jurassic sauropod), and four Permian early tetrapod individuals, *Cacops*, *Eryops*, *Varanops*, and *Captorhinus*.

## Materials and methods

We collected *Edmontosaurus* post-cranial elements of rib, vertebrae, and scapula at the Hell Creek Formation in Glendive, MT, and limb bone elements from *Camarasaurus* at the Morrison Formation in CO. We subjected them to fixation in formalin at the site for transport to the lab. We also secured museum limb specimens of *Cacops*, *Eryops*, *Varanops*, and *Captorhinus* from the Oklahoma Sam Nobel Museum of Natural History. These were fixed in formalin upon arrival. Bones were rinsed in pure water, then air-dried, and ground thin sections were made to 40 and 80-micron thickness on glass slides. Sections were examined without coverslip under reflected light UV fluorescence microscopy<sup>2</sup> for the presence of auto-fluorescing clots within microvascular bone canals.

Most clots presented as uniformly dark masses under brightfield microscopy, often filling the canal lumen, except for Permian specimens, which appeared diffuse in comparison. Crystalline shaped structures were evident in all clots, however (figures 1a, 2a, 3a, 4a, 11a).

All clots autofluoresced brightly under UV illumination (275–290 nm), indicating massive presence of iron—probably from remains of heme in blood from the once-present vasculature (figures 1b, 2b, 3b, 4b, 5b, 6b, 7b, 8b, 9b, 10b, 11b, 12b). Permian specimens were less reactive in UV fluorescence, probably because they were fixed and dehydrated long after removal from deposits, but also because they exhibit thinner compact bone. We fix our specimens at the deposits to retard any potential degradation post-removal. Despite environmental factors (erosion, water infiltration, annual freeze-thaw cycle) and predation by bacteria, fungi, microbes, worms, and rodents over a substantial period of time, clots adhered tenaciously to bone matrix walls and often completely occluded blood canals the entire depth of our sections (both thick and

thin). We were shocked that intense mechanical vibration during grinding and polishing for thin sectioning did not dislodge clots from canals.

We also cut rectangular planks of Permian bone and partially decalcified them in EDTA, which exposed solid tubes of clots extending several millimetres from the remaining undecalcified bone (unpublished results).

Clots adhered unwaveringly to microvascular bone canals and were characterized by embedded, dark and non-fluorescing crystallized objects surrounded by the brightly fluorescing iron signal (figures 1b, 2b, 3b, 4b, 5b, 6b, 7b, 8b, 10b, 11b, 12b, 13b). Clots did not infiltrate into bone (figures 1b, 2b, 3b, 6b, 8b, 10b, 11b, 12b, 13b, 14b, 15), thus any tissues buried deeply in bone matrix (osteocytes, long canalicular filopodia, collagen) were unperturbed by iron.

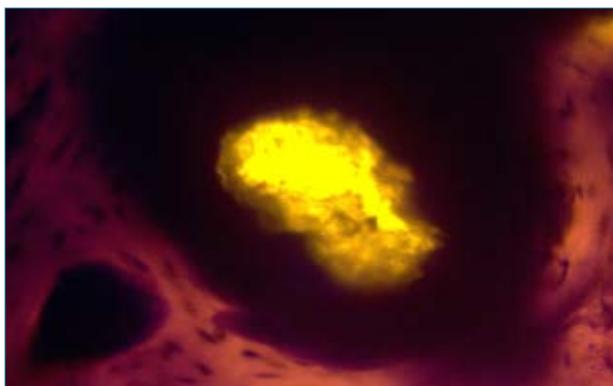
We examined clots on a Hitachi SU3900 SEM in BSE mode and performed elemental analysis. Clots returned a very bright backscattered electron signal, strikingly like the autofluorescence images in UVFL (figure 15). The BSE image confirms that clots did not infiltrate the bone, except for minimal intrusions into very small cracks. EDS confirmed that clots were high in calcium, iron, and oxygen, and were phosphorus rich (figure 15) and lacked significant presence of aluminum, carbon, chlorine, magnesium, manganese potassium, sodium, silica and sulfur (unpublished results).

## Discussion and conclusions

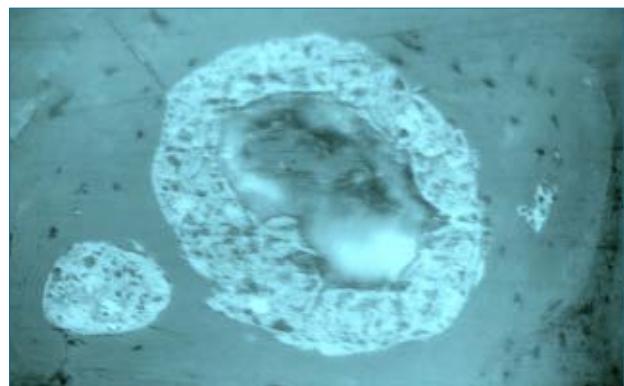
We reason that the astonishingly persistent clotted microvascular bone canals observed in these specimens are characteristic of disseminated intravascular coagulation (DIC) or hypercoagulopathy, a process that results in clotting of blood throughout the vascular system as a result of severe trauma.<sup>2,5–8</sup> Systemic clotting leads to obstruction of blood vessels, organ failure, and death.

All thin sections are 40 microns thick, and magnification is 250X.

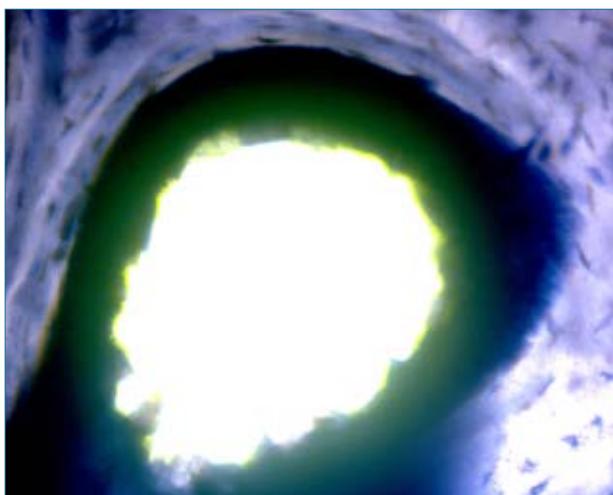
UVFL = ultraviolet fluorescence; HC = Hell Creek formation, MT; MO = Morrison formation; CO, LP = Lower Permian; OK; SN = Sam Nobel Museum, OK.



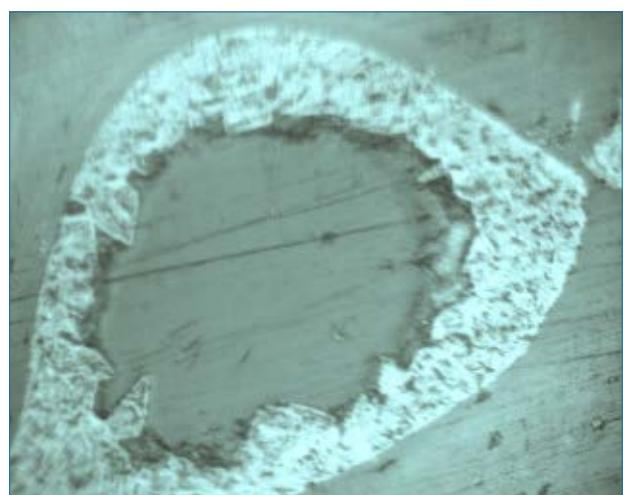
**Figure 1a.** *Edmontosaurus* rib, #DSTRI-5622B. Brightfield image, collected HC deposit, MT



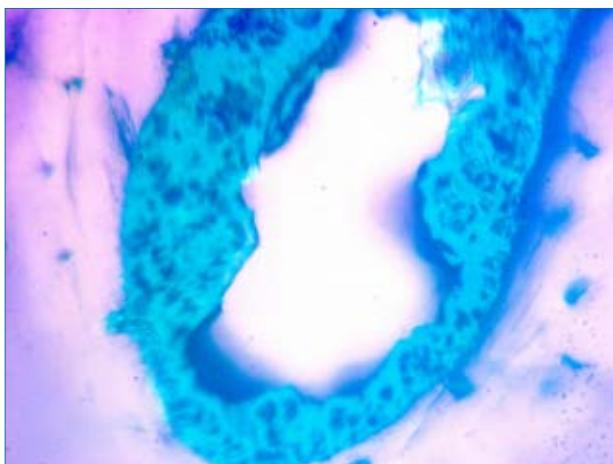
**Figure 1b.** *Edmontosaurus* rib, #DSTRI-5622B. UVFL image



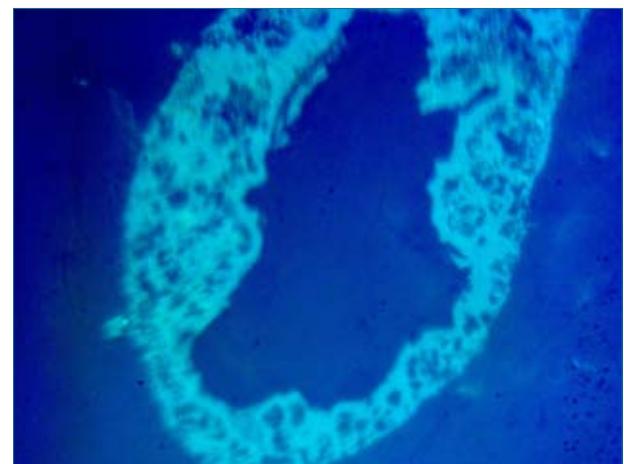
**Figure 2a.** *Edmontosaurus* scapula, #DSTRI-5622E, Brightfield, collected HC deposit, MT



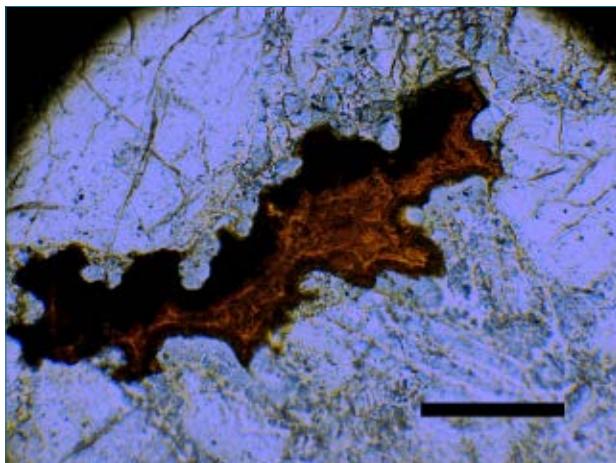
**Figure 2b.** *Edmontosaurus* scapula, #DSTRI-5622E UVFL image



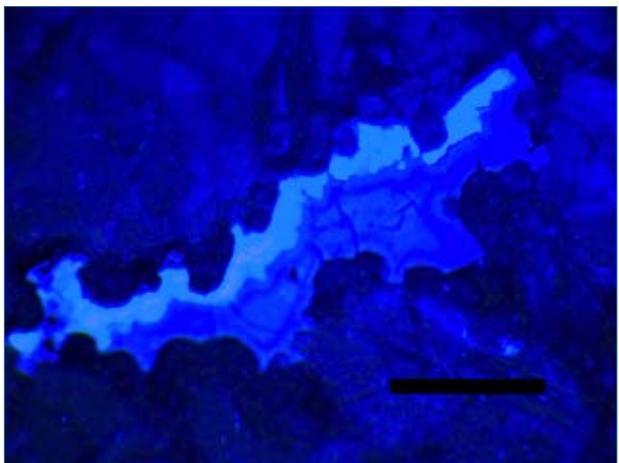
**Figure 3a.** *Nanotyrannus* vertebra, #DSTRI-91C, Brightfield image, collected HC deposit, MT



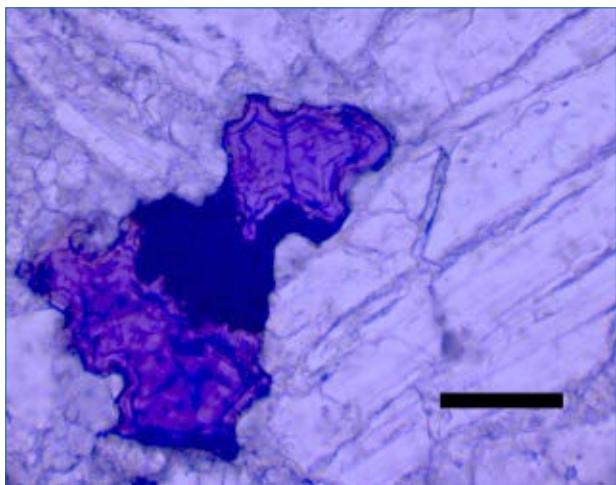
**Figure 3b.** *Nanotyrannus* vertebra, #DSTRI-91C, UVFL image



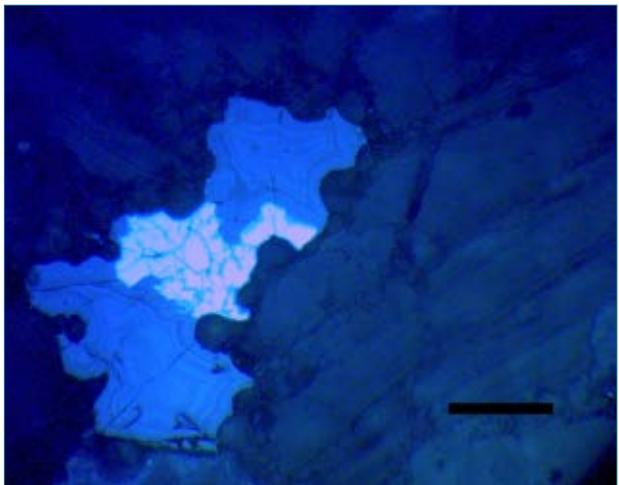
**Figure 4a.** *Camarasaurus* limb, #DSTR-9420, Brightfield/FL image, MO, OK



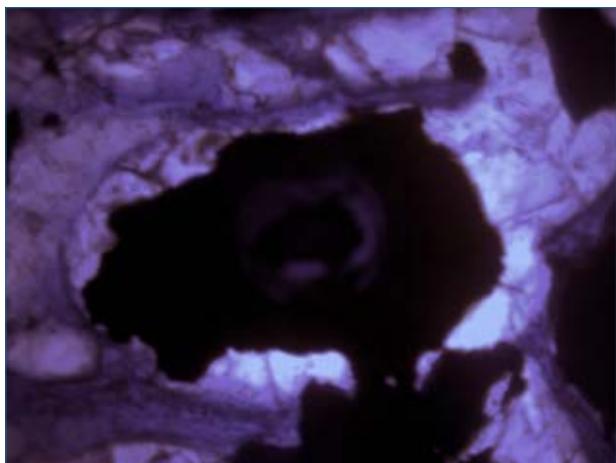
**Figure 4b.** *Camarasaurus* limb, #DSTR-9420, UVFL image collected



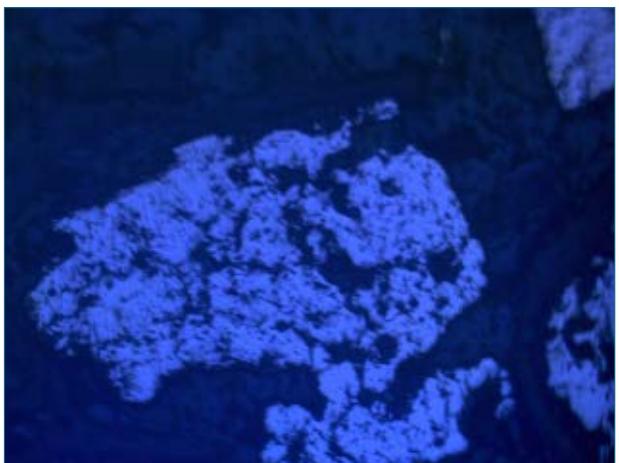
**Figure 5a.** *Camarasaurus* limb, #DSTR-9421, Brightfield image, collected HC deposit, MT



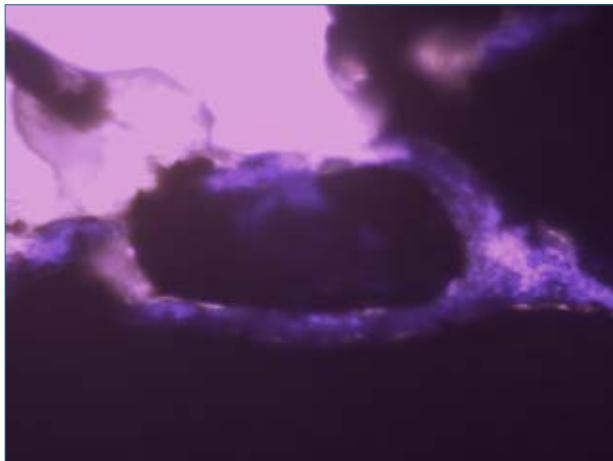
**Figure 5b.** *Camarasaurus* limb, #DSTR-9421, UVFL image



**Figure 6a.** *Cacops* humerus, #DSTR-6923, Brightfield image, collected SN Museum, OK



**Figure 6b.** *Cacops* humerus, #DSTR-6923, UVFL image



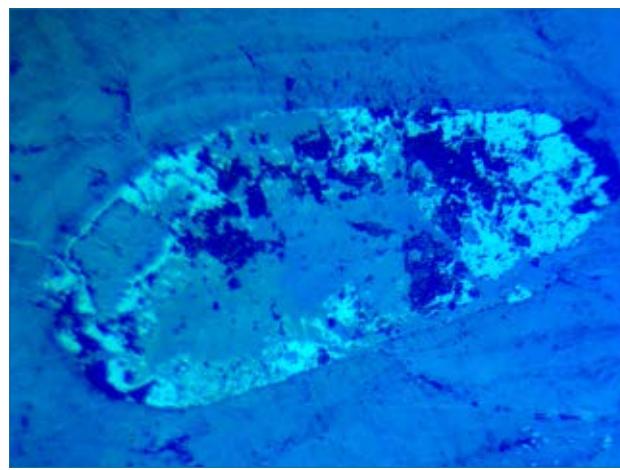
**Figure 7a.** *Cacops* humerus, #DSTRI-6923, Brightfield image, collected SN Museum, OK



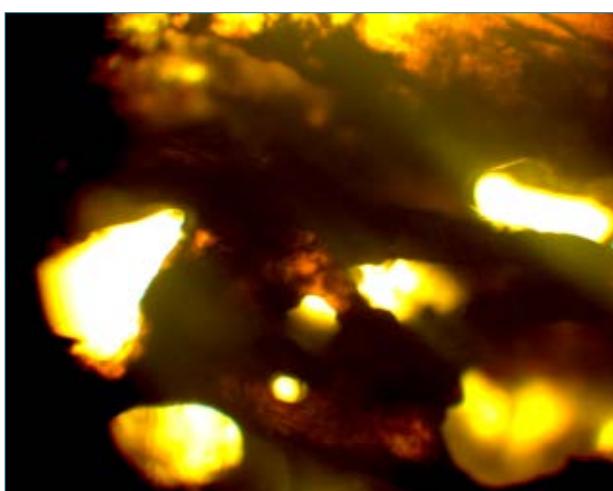
**Figure 7b.** *Cacops* humerus, #DSTRI-6923, UVFL image



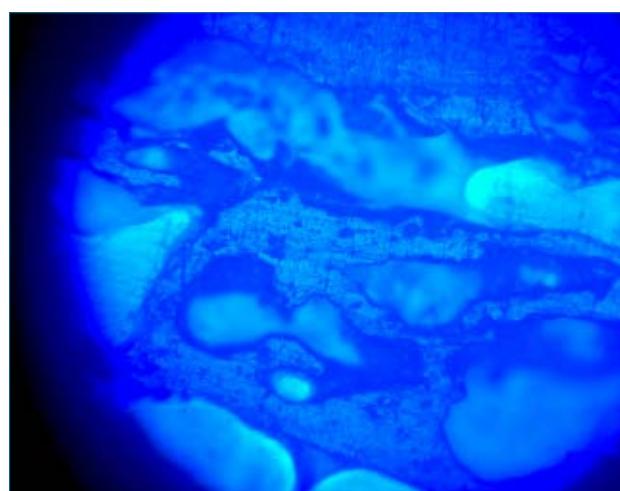
**Figure 8a.** *Eryops* humerus, #DSTRI-11223, Brightfield image, collected SN Museum, OK



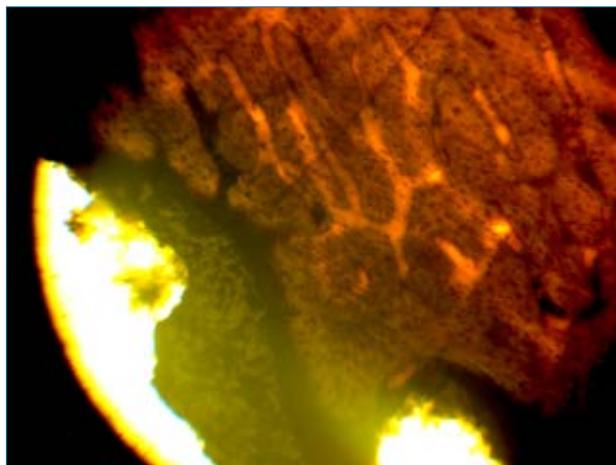
**Figure 8b.** *Eryops* humerus, #DSTRI-11223, UVFL image



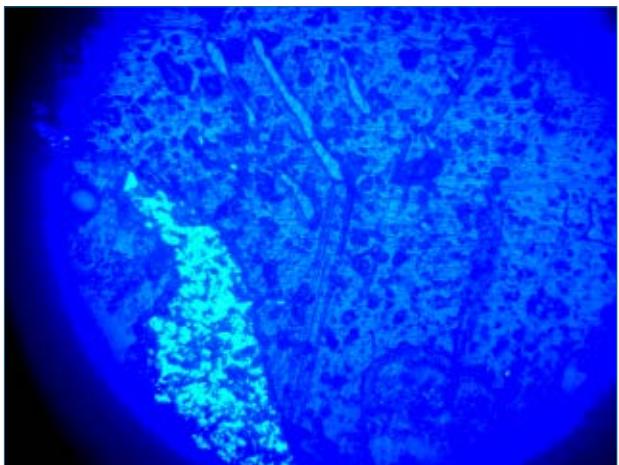
**Figure 9a.** *Varanops* femur, #DSTRI-11323, Brightfield image, collected SN, OK



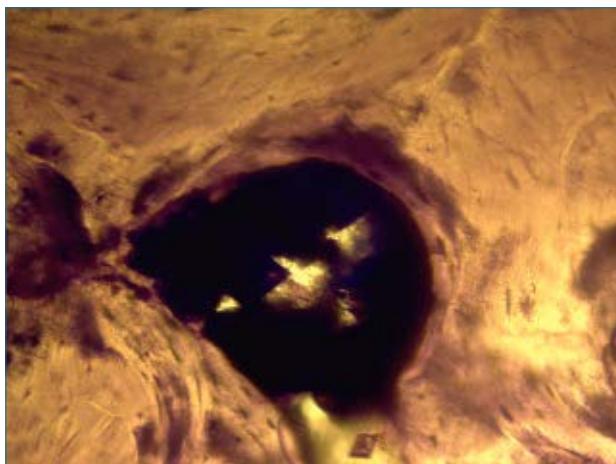
**Figure 9b.** *Varanops* femur, #DSTRI-11323, UVFL image



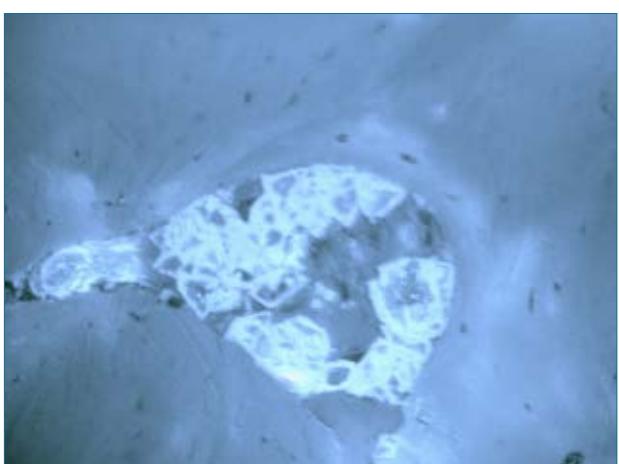
**Figure 10a.** *Captorhinus* humerus, #DSTRI-11423, Brightfield image, collected SN, OK



**Figure 10b.** *Captorhinus* humerus, #DSTRI-11423, UVFL image



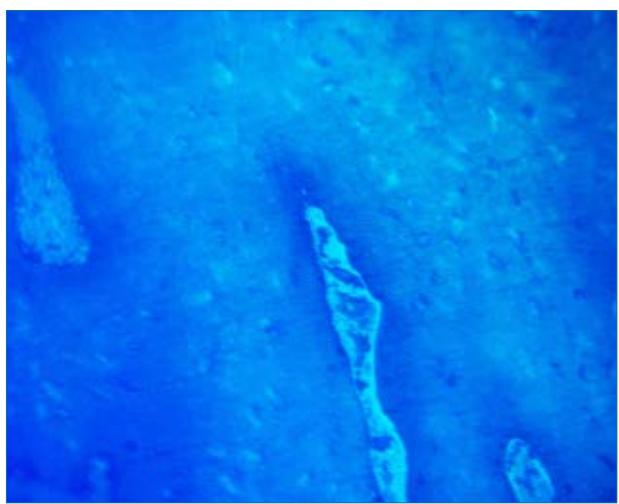
**Figure 11a.** *Dimetrodon* femur, #DSTRI-54G, Brightfield image, collected LP, OK



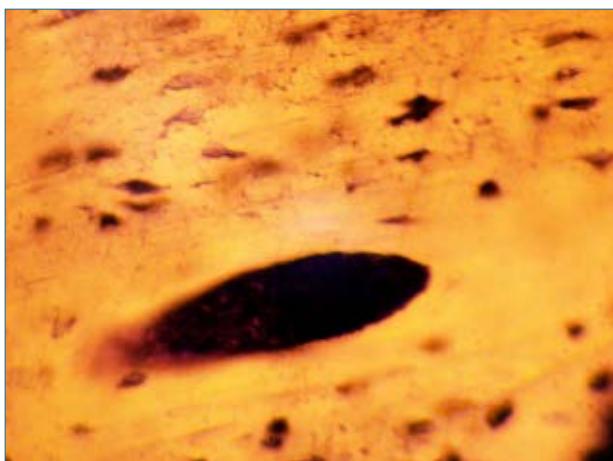
**Figure 11b.** *Dimetrodon* femur, #DSTRI-54G, UVFL image



**Figure 12a.** *Dimetrodon* jaw, #DSTRI-54J, Brightfield image, collected LP, OK



**Figure 12b.** *Dimetrodon* jaw, #DSTRI-54J, UVFL image



**Figure 13a.** *Dimetrodon* rib, #DSTRI-54K, Brightfield image, collected LP, OK



**Figure 13b.** *Dimetrodon* rib, #DSTRI054K, UVFL image



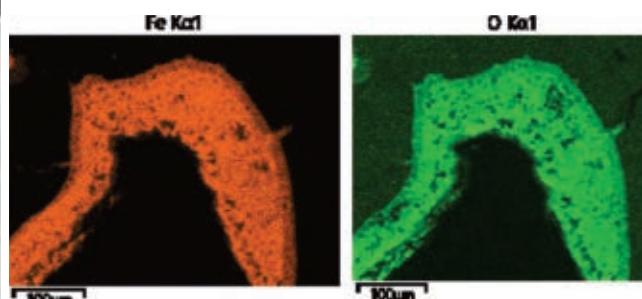
**Figure 14a.** *Dimetrodon* rib, #DSTRI-54K, Brightfield image, collected LP, OK



**Figure 14b.** *Dimetrodon* rib, #DSTRI054K, UVFL image



**Figure 15.** *Triceratops* vertebra #DSTRIHCTV22, SEM, BSE image, collected HC MT



Reports generally indicate that DIC develops due to severe trauma, acute injury, sepsis, cancer, leukemia, aneurysms, infections, and complications with obstetrics and other conditions, even Covid-19.<sup>5-8</sup> Our conclusion is that death by drowning is indicated by these microvascular clots.

A direct challenge to our conclusion is noted.<sup>9</sup> That author failed to note that our work in 2013 presented the first ever SEM micrograph of a clearly crystallized blood clot in a dinosaur bone blood vessel (*Triceratops* horn).<sup>10</sup>

Additionally, we published a higher resolution SEM micrograph of a *Triceratops* clot within a vessel in 2015 showing fine detail of the clotted blood products.<sup>11</sup> These crystalline clots show no evidence of infill from the surrounding soil matrix. One could argue that they are simply crystallized calcite, however the elemental map of a *Triceratops* vascular crystalline clot shows otherwise (figure 15).

Also, we have observed clots in histological reports of Permian amphibian bone thin sections and have commented accordingly.<sup>4</sup> Furthermore, we also recognize clots in dozens of reports of dinosaur bone histology.<sup>12-23</sup>

Senter,<sup>9</sup> provides a list of causative factors for DIC similar to those listed above, and includes others like cardiovascular disease, anemia, and heat stroke. He concludes that this “means that DIC is not diagnostic of drowning.” However, the link between DIC and asphyxia/drowning is certainly supported. One recent study lamented “no study has investigated coagulopathy following drowning”, and found that 80% of patients with drowning-induced asphyxia developed overt DIC within one day after hospitalization. They concluded, “Overt DIC occurs in the vast majority of drowning patients.”<sup>6</sup>

It is also well established that humans resuscitated in the E.R. after a traumatic drowning event experience profuse bleeding, since clotting factors are exhausted during the trauma event.<sup>5,6</sup> Senter makes note of this profuse hemorrhaging presented by drowning victims and states, “the kind of DIC that drowning causes ... [means that] clots that begin to form are immediately destroyed so that a patient’s blood cannot clot.”<sup>9</sup>

This betrays the fact that most DIC reports are in the *medical* literature, specifically related to *human patients* who have been *rescued* from a drowning event and are *being treated* in the emergency room when they present with hemorrhaging. It is likely that treatment began the very moment they were rescued. Humans don’t drown in the E.R., and no dinosaur was rescued or ever received transfusions, heparin, or CPR.

The medical literature on this subject cannot adequately explain the conditions which produced the abundant clots

we observe in vertebrates buried at Hell Creek, especially with the obvious benefits of medical therapies employed to save humans from near-death drowning events. Additionally, the literature is unclear if resuscitation of human drowning victims impacts the onset of profuse bleeding, or if hemorrhaging is a natural consequence after acute traumatic systemic thrombosis, as Senter surmises.<sup>9</sup>

In the case of the bones studied here, no profuse bleeding seems to have occurred post-mortem because most of the microvascular canals are still fully obstructed by clots that did not dissolve. Furthermore, the clots remain unperturbed to this day and seem impervious to the mechanical vibrations of sectioning and polishing.

The typical death scenario for dinosaurs presented in the paleontology literature relies on natural causes of death prior to burial in sediments.<sup>24</sup> This scenario even anticipates mineralization of bone during the burial process.<sup>24</sup> Most of the dinosaur bones we have removed from deposits are still bone (thus are non-mineralized). They behave as modern bone during standard decalcification, practiced routinely in hospital histology labs. Moreover, the tissues we recover after decalcification take up standard tissue and nucleic acid stains, and are surprisingly pliable.

If buried dinosaurs died by natural means, blood would have pooled to the decumbent part of the body (*livor mortis*) thus clots or pooled blood should be *absent* in skeletal elements closer to the surface than other (deeper) bones in the same buried animal. The presence of systemic clots throughout these skeletal remains points strongly to a traumatic event leading to clotting of blood within microvascular bone canals during a drowning event, and not a death characterized by postmortem blood pooling.<sup>2</sup>

The fact that systemic bone clots are found in specimens that are considered to be in deposits ranging in conventional ages of 65 million to 290 million years suggests that this was one mass burial event.

As mentioned, histological studies of dinosaur bone feature thin sections to illustrate bone physiology and growth. Paleontology workers must undertake an examination of those specimens using UV autofluorescence microscopy to identify the presence of thrombosis in dinosaur microvascular canals, which we recognize as clots. This could extend the range and prevalence of clots across taxa and deposits globally. It might also confirm that *livor mortis* was unlikely in death due to asphyxiation and disseminated intravascular coagulation.

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# The evolution of sweat glands stymies evolutionists

*Jerry Bergman*

The main means by which humans cool their body is by sweat glands. For humans, only a few degrees above normal body temperature can be lethal, thus, for us, sweat glands are essential for life. The anatomy, physiology, and evolution of sweat glands is briefly reviewed. The review highlights the inherent complexity of the sweat gland cooling system. Although temperature regulation is a critical consideration in evolution, no progress has been made towards a viable explanation of the evolution of these systems in the past century.

No cold-blooded animal has sweat glands (figure 1); only warm-blooded animals and humans do. In fact, “One of the most distinctive physiological traits differentiating humans from other primates is a reliance on sweating to cool off.”<sup>1</sup> Humans have two main sweat gland designs, the eccrine and the apocrine types (figure 2).<sup>2</sup> Both have a temperature-regulation function. And both types also have an important excretory function, similar to the kidney, helping to clear from the body excess micronutrients, metabolic waste, and toxicants.<sup>3</sup>

## Eccrine sweat glands

Eccrine sweat glands are coiled, tubular glands which are present throughout almost the entire human skin surface. The exceptions include the vermillion border of the lips, the external ear canal, nail beds, glans penis, clitoris, and labia minora. In the eyelid, eccrine glands are found at the lid margin and on the dermis surface. In the embryo, eccrine sweat glands first appear on the palms and soles during the fourth month of gestation. They become functional soon after birth. Eccrine sweat consists largely of water and NaCl, plus a mixture of chemicals originating from the interstitial fluid. In addition to sweat glands, the skin that covers most of the body contains hair follicles, hair arrector muscles, and sebaceous glands which produce an oil to help maintain the quality of the hairs.<sup>4</sup>

## Apocrine sweat glands

In contrast to eccrine and sebaceous glands, apocrine sweat glands are odiferous glands that are responsible for what most humans regard as an unpleasant odour. Apocrine glands produce viscous, lipid-rich sweat containing proteins, sugars, and ammonia.<sup>5</sup> The unpleasant odour comes from the activity of certain skin bacteria decomposing this fluid.

In many species the analogous glands act as scent glands, producing and releasing pheromones.<sup>3</sup> A pheromone is a hormone-like chemical that a creature produces to affect the behaviour of another of the same species.

Apocrine glands open into hair follicles, leading to the skin surface. These large-branched glands are mostly confined to the axillary and perineal regions of the body. They include the perianal region, the labia majora in women, the scrotum and prepuce in men, the axillae (armpits), and a small number are located on the scalp, abdomen, and chest. They are also located around the nipples and areolar tissue surrounding the nipples.<sup>6</sup> Apocrine sweat glands become functional when stimulated by hormones at puberty.

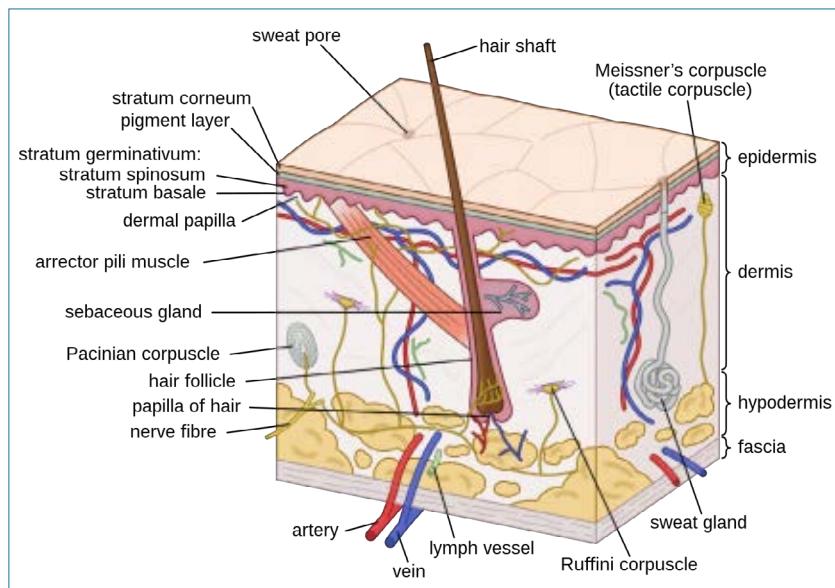
## Apoeccrine sweat glands

The apoecrine glands, discovered only in 1987, are similar to the eccrine sweat glands. Located in the axillary and perianal region they appear between the ages of about 8 to 14 years. The number increases to as high as 45% of the total axillary glands by age 16–18. They likely serve as sweat glands and probably produce secretions that function as pheromones. As stated above, pheromones are chemicals secreted in sweat and perceived by another individual of the same species, often females. For example, androstanedione is present at higher concentrations in male than female sweat, and is easily detected by women.<sup>7</sup> These pheromones are believed to function as sex attractants.

## Eccrine sweat gland importance

All mammals have the apocrine type of sweat glands, though other than in a handful of species including horses, these do not play a significant role in cooling the body.<sup>8</sup>

All mammals also have the eccrine type of sweat glands, which open directly onto the skin’s surface. In most,



**Figure 1.** Cross-section of human skin showing a sweat gland (on the right in grey)

however, they are confined to the hands and feet and do not play a significant role in thermoregulation. All catarrhine primates (which includes humans and the Old World apes and monkeys) have them over most of the body. (A couple of species of New World monkeys have them over the body as well, which does not fit the neat evolutionary story of common ancestry, so this is naturally regarded as coincidental ‘convergent evolution’.)

The density of these sweat glands in humans is uniquely high; fully eccrine glands are the dominant human skin appendage, with densities exceeding 200 glands/cm<sup>2</sup> in regions such as the face.<sup>1</sup> This high density, some ten times that in chimpanzees and macaques, is unique to humans. In all, depending on one’s total skin area, which varies with height and breadth, humans have between two and five million sweat glands.

Eccrine glands are important because “The evaporation of sweat is the major mechanism by which humans dissipate body heat, and humans have thermally induced sweat rates that are 4 to 10 times higher than those of chimpanzees, secreting 1 L or more of sweat per hour.”<sup>1</sup> “The effectiveness of human thermoregulatory sweating” is due to a dramatically larger “density of water-secreting eccrine sweat glands in human skin relative to that of other primates.”<sup>1</sup>

As a result, humans must rely on sweating to cool off far more than other primates.<sup>1</sup> In hot environments, water evaporation cools by shedding excess heat, either by sweating, as in humans or by many short quick breaths called panting. Many mammals and all birds pant.<sup>9</sup> Cool air from panting comes into contact with the moist lung lining and

throat, lowering body temperature. The cool air also causes water evaporation from the tongue and throat as well as the lung lining, all helping to cool the body. In contrast to sweating, panting produces heat from the muscular activity required to create the increased air flow across the mucous membranes.<sup>10</sup> Chimps use sweating for body cooling to some extent, but nowhere near as much as humans do. Instead, in contrast to humans, they use panting to a significant degree.

### Thick hair of mammals

With rare exceptions, such as the naked mole rat, mammals are covered with thick hair called fur. Fur greatly reduces airflow over the skin, consequently mammals, including

non-human catarrhines like chimps, must use other means to reduce body heat to prevent overheating. Some mammals, including horses, monkeys, apes, dogs, and mice have localized sweat glands on their hooves or paws. Since humans are furless, the sweat evaporation from their high density of eccrine sweat glands in their skin, producing copious amounts of sweat is very effective in causing evaporative cooling as the water in the sweat evaporates.

### The anatomy of the sweat gland system

All three types of sweat glands require a complex support system, all of which must exist and be properly designed for them to function.<sup>11</sup> First, the specially designed cells that secrete the sweat must themselves exist. Then the ducts that deliver the sweat to the skin must be designed and constructed. The nerve control of sweat production, which includes, for example, the hippocampus for emotional sweating and hypothalamus for thermal sweating, must be designed, constructed, and functional. Also required is the arterial and venous system to supply fresh blood and carry away metabolic waste products from the sweat glands.

One of the most important designs is the sweat feedback system. When the body sensors detect abnormally high body temperature, the temperature regulatory centre of the brain is stimulated to activate the sweat glands to bring the body temperature down. When body temperature reaches the normal range, the feedback ends the cooling process. The thermostat used in a room air conditioner is a good analogue to the body’s feedback system—it both turns on the compressor, and when the temperature is

down to the level required, turns it off. The entire feedback loop involves a direct effect on the sweat glands via nerves connected to them at the neuroglandular junction, as well as involving peripheral thermal receptors and the central nervous system.<sup>12</sup>

The problem for evolution is that most thermoregulation mechanisms require a complex network of special receptors, both internally and externally, plus nerves, muscles, respiratory, circulatory and hormonal control sites, as well as organs such as the heart, the brain, and the preoptic area (the anterior part of the hypothalamus) to function. Sweating is a complex system controlled by the hypothalamus and the nervous/hormonal system.<sup>13</sup>

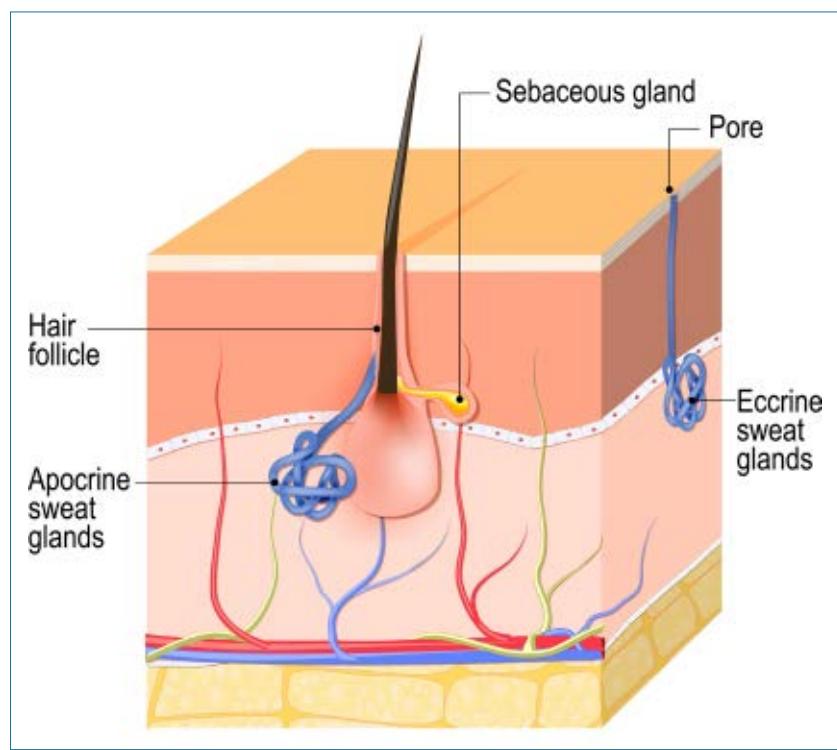
### Sweat glands regulate electrolyte balance and pH

Sweating regulation is also a critical part of the body's system of regulating electrolyte balance, or at the least, responding to electrolyte imbalance. The sweat glands are part of the mechanism required to regulate electrolytes, and also to help in regulating the pH (acid-base balance; a low pH level or high acidity is caused by too many H<sup>+</sup> ions and a high pH level is caused by too many OH<sup>-</sup> ions).

The intracellular pH range for animal cells, depending on the cell, is 5.5 to 6.8. If the pH levels deviate too far from this range, coma can result.<sup>14</sup> To complicate the issue further, different body fluids require different pH values. The blood must maintain a very tight range of between 7.35–7.45. Even minor deviations from this range can have severe health implications. The pH of saliva ranges from 6.5 to 7.5. After swallowing, the food reaches the stomach where upper and lower parts of the stomach require different pH values to function. The upper part has a pH of 4–6.5, while the lower part is highly acidic with a pH of 1.5–4.0. The partly digested food then enters the intestine, which is slightly alkaline, with a pH of 7–8.5. Maintaining the pH values of different regions is critical for their function.

Sweat glands are believed to play a part in pH balance by several mechanisms, including sodium ion regulation, reabsorbing bicarbonate ions, and possibly by direct secretion of hydrogen ions into the duct before the sweat is released onto the skin surface.<sup>15</sup>

Electrolyte regulation is critical because its imbalance can cause heart arrhythmia, kidney problems, and, in



**Figure 2.** Eccrine and apocrine sweat glands in human skin

Image: Tetiana Zhabska / Alamy

extreme cases, death.<sup>16</sup> The complexities of the system were highlighted by research of sweat gland functions:

"In sweat glands, salt excretion and reabsorption are regulated to avoid electrolyte imbalance. To date, the mechanism underlying such regulation is not fully understood. Corin is a transmembrane protease that activates atrial natriuretic peptide (ANP), a cardiac hormone essential for normal blood volume and pressure. Here, we report an unexpected role of corin in sweat glands to promote sweat and salt excretion in regulating electrolyte homeostasis."<sup>12</sup>

The genetic basis for sweat gland function, "one of the most extreme and distinctively human traits",<sup>17</sup> has now been detailed. Researchers also claim that they have "discovered how this distinctive, hyper-cooling trait evolved in the human genome."<sup>21</sup> The study measured the expression level of the *Engrailed 1* (*EN1*) gene in humans which determines eccrine gland density. The *EN1* gene in turn encodes a transcription factor protein which, in the embryo, is part of the genetics that directs the construction of eccrine glands. Due to this finding, "Kamberov and colleagues hypothesized that perhaps one way in which humans could have built more sweat glands in their skin is to evolve genetic changes [mutations] that increased the production of *EN1* in the skin."<sup>1,17</sup>

The *EN1* gene is affected by the nearby DNA enhancer region called *hECE18*, which boosts *EN1* production in the

skin to cause the development of more eccrine glands. The researchers then determined that the human version of the hECE18 gene is more active than that of ape or macaque versions. Given the evolutionary assumption, they assumed that mutations in this and other genes caused the evolution of the abundance of human eccrine glands.<sup>18</sup> This assumes that modern primates have the same gene set that the claimed chimp and human common ancestor also had.

### Evidence for evolution

Evolution is assumed to be responsible for the design and development of the temperature regulation and sweating systems, but this belief is rarely described or defended. It is only assumed. The evolutionary belief is that the thick hair, called fur, on the putative evolutionary ancestors of humans slowly disappeared. Sweat glands, or at least their current high density in humans, developed concomitantly. One theory is that a hairless mutation occurred in the last chimpanzee/human common ancestor 6 million years ago.<sup>19</sup> All humans allegedly now have this hairless mutation which, so far, has not been identified.

The problem is that hair loss by mutation is not a gradual process, so this would have required eccrine glands to be already all over the body, and in high enough densities to take over from the ape thermoregulation system almost instantaneously. This is because electrolytic and thermal regulation is critical and would have needed to be maintained within very strict limits to survive this proposed transition.

The problems of how temperature-regulating mechanisms in general are supposed to have evolved are commonly sidestepped. A leading text on the regulation of temperature credits evolution with having “produced a wide variety of adaptive strategies and tactics to exploit or deal with this variable environmental factor.”<sup>20</sup> But after noting that “behavioural and physiological responses to temperature change [are] critical to an understanding of the survival and evolutionary fitness of animals in a thermally variable and unpredictable environment,” the 37 mentions of evolution in the text never attempt to explain how, why, or when these critical-for-life structures developed.

A similar situation prevails in newer literature on temperature regulation in animals.<sup>21,22</sup> Evolution is said to have selected for the higher density of eccrine sweat glands in human skin, making humans’ copious sweat production possible.<sup>23</sup> But after such outlines, little or nothing is said in texts describing gland evolution about *how* these changes could occur in a slow, gradual Darwinian fashion. This situation in the literature is not confined to explanations for the evolution of human sweating, but extends to the other aspects of temperature regulation in general.

By way of aside, some have attempted to place a time on when the evolution of warm-bloodedness in mammals occurred,<sup>24</sup> but this has been disputed by others for good reasons.<sup>25</sup>

A 2009 text mentions evolution 83 times and follows the same pattern, ignoring the details of *how* this evolution could have occurred to allow the creature to survive during the transition.<sup>22</sup>

Their conclusions about the evolution of human sweating means of temperature control are derived not from facts or even ‘just-so’ stories, but from the belief that humans and modern chimpanzees evolved from an ape-like common ancestor. Since evolutionists have no evidence of that common ancestor, it is assumed to be similar to the modern chimp.<sup>26</sup> Then comparing the number of sweat glands in primates with the number in humans, it is concluded that humans evolved a larger number of sweat glands.<sup>27</sup>

Likewise, genetic comparisons of sweat regulation between humans and nonhuman primates reveal differences, and the conclusion is made that the differences are due to mutations, for example:

“...the accumulation of human-specific mutations in a developmental enhancer collectively promoted the production of eccrine glands in humans by up-regulating the expression of the *Engrailed 1* transcription factor in the skin.”<sup>1</sup>

### Summary

The evolution from fur to sweat-gland cooling is considered by evolutionists to be one of the most important evolutionary events in human history.<sup>28</sup> Sweat gland evolution is a concern expressed ever since Darwin discussed the topic in his *Origin of Species*.<sup>29</sup> Evolutionists have also conceded that metabolically based maintenance of “relatively stable body temperature in the face of greatly fluctuating ambient temperature is among the most remarkable attributes of mammals and birds.”<sup>30</sup> They believe that this remarkable attribute evolved in mammals about 233 million years ago in the Late Triassic.<sup>31</sup>

Part of the reason for the difficulty in explaining the evolution of the different thermoregulation systems is because all known temperature regulation systems are part of the body’s complex nervous, hormonal, hypothalamic, muscular, glandular, venous, and arterial systems.<sup>32</sup> Sweating is a complex system finely regulated by the hypothalamus and the nervous/hormonal system.<sup>13</sup> The entire system must be functionally integrated to maintain the required narrow body temperature above the hypothermal lower limit, and below the hyperthermal upper limit. And until this system is functional to effectively maintain this narrow range, human life is not possible.

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**Jerry Bergman** has nine academic degrees, including five masters and two Ph.Ds. His major areas of study for his graduate work include anatomy and physiology, biology, chemistry, and psychology. He has graduated from Wayne State University in Detroit, Medical University of Ohio in Toledo, University of Toledo and Bowling Green State University. A prolific writer with over a thousand publications to his credit, including 43 books and monographs, Dr Bergman has taught biology, microbiology, anatomy and physiology, chemistry, biochemistry, geology, astronomy and psychology at the college level. Now retired, he has taught at The University of Toledo Medical College, The University of Toledo, Bowling Green State University and other schools for a total of close to 50 years.

# No evidence for heart evolution

Jerry Bergman

The heart is one of the major organs without which mammals cannot survive for very long. This is because the heart pumps blood through the circulatory system which distributes blood throughout both the pulmonary and systemic circuits. The dominant evolutionary belief is that the heart, the “most vital of all organs is a product of evolution and has spent millions of years perfecting itself to keep humans alive. Scientists look at other animals to observe how they believe the human heart evolved to its current state.”<sup>1</sup> In other words, no direct evidence of heart evolution exists, and a study of the hearts of living animals is the only way that an evolutionary theory can be created. This review discusses hearts in living animals in order to evaluate the viability of this subjective view.

**T**he heart-evolution literature often gives a timeline of the prevailing evolutionary story but provides no evidence for the actual alterations required to evolve from a single-tube heart to a four-chambered heart.<sup>2</sup> Typical is the following:

“The first heart-like organ appeared in our biological history over 500 million years ago … from a single-layered tube with own contractility supporting an open circulatory system, to a powerful four-chambered muscular pump devoted to loading and unloading a large amount of blood around a closed, valved circuit circulatory system. The vertebrate heart is biologically specific to a species and is the product of millions of years of fine tuning.”<sup>3</sup>

This quote summarizes the prevailing evolutionary theory of heart evolution but provides no evidence for the changes. Nor does it attempt to explain how one heart type could evolve into another design *and* allow the organism to thrive during the transitions. In this example, even just-so stories of the details were not postulated. In short, the heart somehow

“… evolved from the early chordate circulatory system with a single layered tube in the tunicate (Subphylum Urochordata) or an amphioxus (Subphylum Cephalochordata), to a vertebrate circulatory system with a two-chambered heart made up of one atrium and one ventricle in gnathostome fish (Infraphylum Gnathostomata), to a system with a three-chambered heart made up of two atria which maybe partially divided or completely separated in amphibian tetrapods (Class Amphibia). Subsequent tetrapods, including crocodiles and alligators (Order Crocodylia, Subclass Crocodylomorpha, Class Reptilia), birds [class Aves] … and mammals (Class Mammalia) evolved a four-chambered heart.”<sup>2</sup>

The most detailed, scholarly article on heart evolution, aptly titled, “Evolution of the heart from bacteria to man”,<sup>4</sup> discussed evolution in general and offered neither evidence,

nor plausible theory, on the specifics of heart evolution from bacteria to man. The main ‘evidence’ of heart evolution reviews is the study of *living* animals which is then extrapolated far back in history.<sup>5</sup>

The first heart is generally assumed by evolutionists to have appeared around 500 million years ago. This structure postulated by Darwinists was a single-layered, pulsating tube that pushed fluids around in an open circulatory system such as in some organisms existing today. An example which details the theoretical mechanism and admits this scenario is speculative writes that the heart

“… evolved by the addition of new structures and functions to a primitive pump. … the evolutionary emergence of hearts with increasing complexity occurred through modification and expansion of an ancestral network of regulatory genes encoding cardiac transcription factors. The expansion of cardiac genetic networks through the duplication of cardiac regulatory genes and the co-option of additional gene networks *probably* allowed for the addition of new accessory structures, such as chambers, valves, and a conduction system, to a primitive vessel-like heart analogous to that of invertebrates and vertebrate embryos. The modular addition of innovations to primitive structures, although *speculative*, has also been proposed as a mechanism for the genesis of other vertebrate organs and body structures. Insights into the genetic circuits that drive the evolution and development of the heart shed light on general principles of organogenesis and evolutionary origins of morphological complexity … [emphases added].”<sup>5</sup>

## Heart structure

The cells in most simple organisms, such as amoebas and diatoms, can absorb enough nutrients through their exterior surfaces, or from other cells, to survive.<sup>2</sup> Larger invertebrates

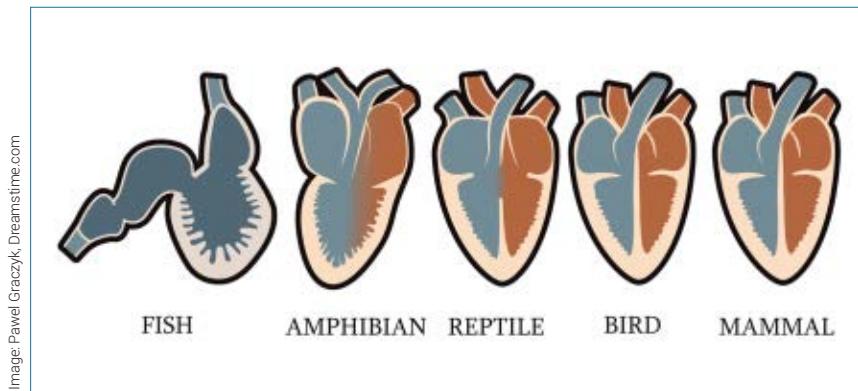
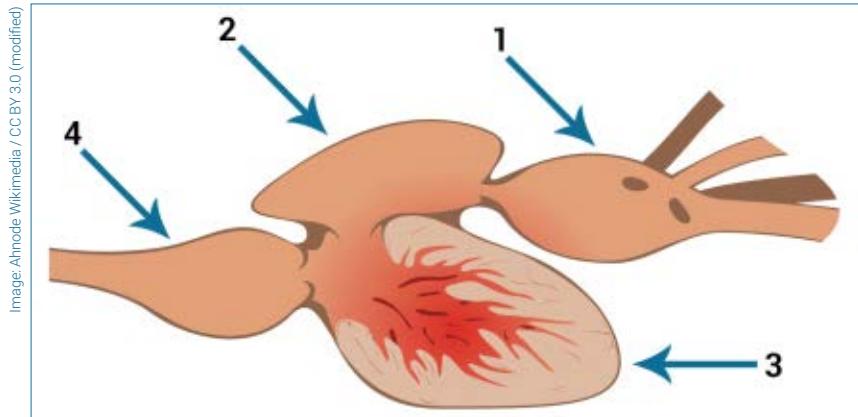


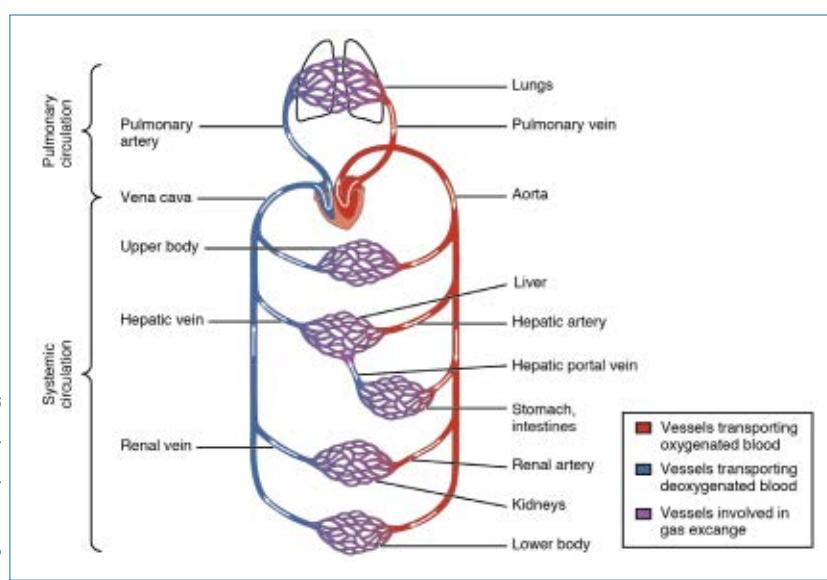
Image: Paweł Graczyk, Dreamstime.com

**Figure 1.** Heart anatomy comparison between fish, amphibian, reptile, bird, and mammal. From IDEA Center 2022.



**Figure 2.** A fish heart diagram. Blood enters 1) the *sinus venosus* at right, then flows through to 2) the *atrium*, before entering 3) the single *ventricle*, which contracts to pump the blood, before exiting into 4) the *bulbus arteriosus*. Despite the four compartments, this is generally described as a 2-chamber heart, referring to the atrium and ventricle.

Image: Anatomy &amp; Physiology, Connexions, Wikimedia / CC BY 3.0



**Figure 3.** Diagram showing the blood flow through the human heart, lungs, and body

use an *open circulatory system* which does not employ blood vessels, or has very few. Examples include arthropods including insects and crustaceans, and most molluscs.<sup>6</sup>

Many aquatic filter-feeding organisms, such as sponges and jellyfish, do not require a circulatory system because the water currents in their environment are sufficient to provide the needed oxygen and nutrients. The more complex bilateral organisms, which include over 1.5 million species, require a closed circulatory system, and thus, consequently, require hearts. For a comparison of the different heart designs see figure 1. The vertebrate heart is believed to be the product of millions of years of fine-tuning which some evolutionists call one of the greatest evolutionary achievements.<sup>3</sup>

Fish hearts (figure 2) draw in deoxygenated blood into a single atrium, then pump it out through a ventricle.<sup>7</sup> This ‘single circulation’ design involves blood entering the heart, being pumped through the gills for oxygenation, then out to the body before re-entering the heart. Blood pressure is comparatively low for oxygenated blood leaving the gills. In contrast to fish, air-breathing land animals use a double circulation design, with a pulmonary circuit and a systemic circuit. The pulmonary circuit moves blood from the heart into the lungs to be oxygenated, and back to the heart before being pumped to the body (the systemic circuit).<sup>8</sup> Deoxygenated blood returning to the heart from the body tissues re-enters the pulmonary circuit. This process, very different from the single circulation used by fishes, requires the much more complex 3- and 4-chambered heart designs.<sup>8</sup>

The amphibian and reptile 3-chambered heart uses a single ventricle to pump blood out of the heart. Consequently, some mixing of oxygenated blood and deoxygenated blood results. The bird and mammal 4-chambered heart is more complex,

but more efficient, because it uses one ventricle for deoxygenated blood, and another one for oxygenated blood, keeping oxygenated blood completely separate from deoxygenated blood.<sup>8</sup>

### Problems for the evolution of the 3- and 4-chambered hearts

At least three subsystems are required for enriching the blood with oxygen. These include (1) lungs or gills, (2) a pumping mechanism (the heart) to transport the blood throughout the body, and (3) a complex network of veins, arteries, and capillaries. All these subsystems, as a unified compatible set, are necessary for life because a closed tube is useless without a pumping mechanism to transport blood, and a pump is useless without the closed circulatory system (arteries, veins, and capillaries) that can carry the blood, which transports nutrients and oxygen throughout the body and also helps eliminate toxic wastes from the body.

### From a 2-chambered to a 4-chambered heart

Given a 2-chambered heart, I could find no viable claims of when, how, or in what lineage, the transition from the 2-chambered fish heart to the far more complex 3-chambered amphibian heart supposedly occurred. This was even the case in journal articles dedicated to this question, such as Bishopric's 2005 paper.<sup>4</sup> This step is a very difficult transition, and presents a challenge for evolutionists even to produce logical just-so stories. The transition requires an effective functional system to keep the organism alive during the entire time of the transition. The changes required to go from single to double circulation include the duplication of the atrium, with the new atrium being fully functional. It also requires the development of a new vein, the pulmonary vein, to take oxygenated blood back into the heart; this complete redesign of how blood leaves the heart and travels to the body requires extensive artery and vein 'replumbing'.

Also mandatory is the modification of the heart muscle for the various chambers to beat in a coordinated fashion and to accommodate the additional atrial fluid pressure changes associated with the modifications. Furthermore, the many nerves, valves, and smaller veins and arteries associated with double circulation, plus changes required in the heart muscle pumping system, must all be redesigned to accommodate this completely new atrium while maintaining the required fluid-pressure balance. The problem, referring to the respiratory system, was explained by one scientist as follows:

"Just how such a different respiratory system could have evolved gradually from the standard vertebrate design ... is, again, very difficult to envisage, especially bearing in mind that the maintenance of respiratory

function is absolutely vital to the life of the organism."<sup>9</sup>

The exact same problem exists with the heart, which is also absolutely vital to life.

### Blood flow in the vertebrate heart

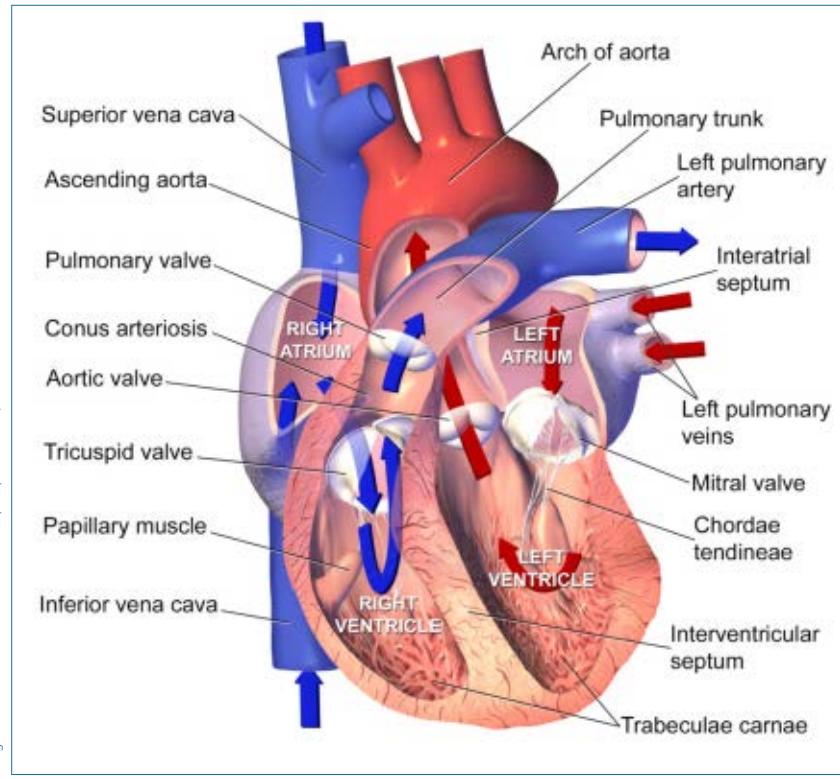
The main parts required for both 3- and 4-chambered hearts include the following (all of which must be integrated into a functional system—see figure 3): Deoxygenated blood returning from the body enters the right atrium (Latin for 'entry hall') of the heart. It then enters the right ventricle which contracts, forcing the deoxygenated blood into the lungs via the pulmonary arteries. Next, the left atrium expands, sucking the oxygenated blood into the left atrium, which then contracts, forcing the blood into the left ventricle. This in turn contracts, forcing the blood into the systemic arterial system to oxygenate the body tissues.<sup>10</sup>

For the pumping system of the 4-chambered heart to function requires proper contraction of the four chambers at the right times. It also requires proper design of the four heart valves, which are: 1) pulmonary, 2) aortic, 3) tricuspid, and 4) mitral (see figure 4). These valves are designed to allow blood to enter the next chamber and to prevent it from re-entering the chamber it had just left. The malfunction of any valve could be lethal. The entire muscle system is controlled by the heart's pacemaker. Electrical impulses from the sinoatrial (SA) node, located at the top of the heart's right atrium, begin the process. The SA node sends electrical impulses at a rate of between 60 to 100 per minute. This rate (and hence the heart rate) may change, depending on physical demands (exercise), emotional stress, or hormonal factors. The response to stress and exercise is mediated by the autonomic nervous system.

If the SA node does not work properly, the heart may beat too fast, too slow, or irregularly, all conditions that create heart problems which, if not treated, can be lethal. When an electrical impulse is released, it causes the upper chambers of the heart (the atria) to contract. The signal then passes through the atrioventricular (AV) node. The AV node responds to the signal by sending it through the muscle fibres of the ventricles, causing them to contract. The messages continue until the heart has progressed through one cycle, then another cycle flows, and so it goes on for the entire life of the individual. Our heart beats about 100,000 times a day or about 35 million times in a year, and 2.5 billion times for an average lifetime.

### The fish heart

As noted above, the fish heart is designed very differently than the 3- or 4-chambered heart. It consists of four separate compartments in a series, the sinus venosus, atrium, ventricle,



**Figure 4.** The human heart showing the major parts

and conus or bulbus (see figure 2 above).<sup>11</sup> Contraction of all these compartments, except the bulbus, causes a unidirectional flow of blood through the heart. Between each compartment are valves causing the blood to flow in one direction only.<sup>12</sup> The bulbus arteriosus connects to the aorta, through which blood flows to the gills for oxygenation. The heart pumps the blood in a single closed loop throughout the body. This design is highly functional for the anatomy and physiology of fish, but would not work for reptiles, amphibians, or mammals.<sup>13</sup> Of all living fish taxa, only the lungfish has a 3-chambered heart.<sup>14</sup>

### No evidence for heart evolution

No evidence exists for heart evolution from a non-heart life-form to a mammal heart. Even evolving from a 2- to a 3-chambered heart (e.g. fish to amphibian) requires far more than the mere duplication of a chamber (the atrium). Changes include a redesign of the:

- veins and arteries surrounding the heart
- interior valves
- interior circuit to connect the heart with the lungs, and
- single circuit connecting to the gills to create a double circuit to connect with the lungs.

No evidence for this imagined gradual evolution of the 3- and 4-chambered heart from the 2-chambered heart exists. The modification of the heart from the 3-chambered heart of amphibians to the 4-chambered heart of mammals requires a change in more than just the septum, the wall between the two ventricles of the 4-chambered heart. No heart septum is employed in the amphibian, part of a septum exists in a reptile, and the complete septum design exists in both birds and mammals. Evolutionists are left to postulate that “This complex but efficient way of getting oxygen and nutrients to body tissues took billions of years to evolve and perfect.”<sup>15</sup> The main difference is the fact that having more chambers enables the heart to pump larger amounts of blood faster.

This general progression of the evolution/complexity of the heart includes many exceptions. For example, the monitor lizard heart is, in some ways, designed like the mammal heart. Also, although reptiles normally have three-chambered hearts, there is one exception, crocodiles. Crocodiles have 4-chambered hearts and a well-developed ventricular septum that completely separates the pulmonary (lung circulation) and systemic (body circulation) sides of the circulatory system. Birds are believed to have evolved from reptiles but, instead of having a heart very similar to reptiles which we would expect if this evolution was true, they have a heart almost identical to mammals.<sup>15</sup> Many evolutionists today believe birds evolved from dinosaurs, and there is some evidence to suggest that at least some dinosaurs, which themselves are supposed to have evolved from reptiles, had a four-chambered heart.

An example where an evolution story is told with no evidence given to document how this evolution could occur, is the following:

“Due to oxygen deficiency and the high metabolic cost of obtaining oxygen from water, vertebrates were forced to make their way out of the ocean and on to land 350–400 Mya. This transition gave the heart a more complex role in terms of blood convection and gas transport. The ability to obtain oxygen straight out of the air called for a redesign of the gas chamber, as the small capillaries inside the gills could no longer function efficiently.”<sup>16</sup>

Conversely, Stephenson noted in a study of the heart that good design is responsible for the heart differences

documented above, writing: “the heart is physiologically specific to the anatomy of each individual species”, but no explanations are given for how this evolution allegedly occurs.<sup>17</sup> No attempt was made to explain how the adaptation of the anatomy of each individual species could have taken place via mutations, and how the transformations could have occurred in a way that would allow the heart to effectively function during this time of change. One respiratory physiology expert, after critiquing the evolutionary scenario, noted that a transitioning from a crocodilian to a bird lung would be impossible, for the reason that the transitional animal would have a hole in its diaphragm. Furthermore, the evidence is clear “that a bird’s radically different system of breathing, in which air is continuously drawn through its lungs, could not have evolved from the hepatic-piston system we see in this theropod dinosaur.”<sup>18</sup> The contrast between the bird heart/respiratory system and that of its alleged ancestors argues against the fanciful reptile-to-dinosaur-to-bird evolutionary scenario.<sup>19</sup>

## Summary

No evidence of heart evolution was found in either the primary or peripheral sources for this review. The current evidence put forward consists largely of the study of living animals and making comparisons of the logical progression from a single-layered pulsating tube to the 4-chambered heart of birds and mammals. The findings in living animals are then dated backwards to produce a hypothetical evolution from the simplest, most primitive system to the most complex design existing today. No effort exists to envision how, or when, those transitions occurred, nor their cause, as well as how one heart could evolve into a more complex design. No detailed effort has been made to document how, or when, those transitions occurred, nor their cause, or how one heart could have evolved from a simpler design into a more complex one.

Furthermore, many animals have such uniquely designed hearts—for example the three-heart system of squid and octopuses, and the multiple ‘hearts’ of earthworms, with 5 pairs of pulsating tubes—that evolutionists conclude they have evolved independently of other heart types.

The odds are essentially zero that several heart designs could evolve separately.

Further, in the standard view, the 4-chambered system evolved from the 3-chambered one three different times (in Crocodylia, Aves, and Mammalia—note that mammals and birds allegedly evolved from very different reptilian stock).

This is another example of the fact that no Darwinian tree exists for hearts. It is clear that common Designer, not common ancestry, best explains the variety of hearts in the living world, each well suited to the needs of the organism. This fact refutes the theory of origin of the heart based on speculative evolutionary transformations that occurred in the unobserved and unobservable past.<sup>20</sup>

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# Irresolvable problems with Neo-Darwinism—experts calling for a new theory of evolution

*Philip B. Bell*

Recently, there have been some surprising confessions from people committed to the prevalent view of origins. This, of course, is neo-Darwinian evolution, the idea that beneficial genetic mutations arising over deep time have provided the raw material for Darwinian natural selection. In this manner, evolutionists say that random errors in the DNA, coupled with the survival of the fittest, have generated every living organism on the planet, from diatoms to dunnocks, yeasts to yaks, and pneumococci to naval architects. The headings in this article are all direct quotations from evolutionists that have appeared recently.

## **"Most of our evolutionary trees could be wrong"**

In June 2022, the University of Bath (UK) issued a press release from Professor Matthew Wills and colleagues, provocatively titled, "Study suggests that most of our evolutionary trees could be wrong."<sup>1</sup> Indeed, their published research in *Communications Biology* really sets a cat among the pigeons.<sup>2</sup>

Over the last 20 years, evolutionary biologists have increasingly had to face the uncomfortable fact that the data of molecular biology often contradict traditional evolutionary family trees. It is well known that the major way in which evolutionists have grouped living creatures has been according to their anatomical similarities. This, in turn, feeds into arguments about homology. Evolutionary scientists usually start with the *assumption* that 'homology' is similarity due to common ancestry.<sup>3</sup> That's their definition, but it is problematic when they then point to anatomical similarities and argue that these are *evidence* for common ancestry. Such arguments for homology are blatantly circular (thus are explanation-free) because they are attempts to prove what had already been assumed!<sup>3</sup>

At the heart of the argument of homology is the idea that similarity of morphology confirms relatedness, but conflicting molecular comparisons among animals are like a spanner in the works. For example, according to research published in 2004, a *morphological* family tree of mammals has the Xenarthra (creatures like sloths, anteaters, and armadillos) as a very 'early' branch of the placental mammals. However, a *molecular* family tree of the same creatures positions the Xenarthra as having evolved 'much later', after a group called the 'Afrotheria'—which includes elephants, tenrecs, golden moles, elephant shrews, hyraxes, aardvarks, and sea cows.<sup>4</sup>

If this isn't striking enough, the latest findings of the Bath research team take things to another level. As well as

analyzing the evolutionary trees of 48 groups of animals and plants (comparing morphological family trees with molecular trees), Matthew Wills and colleagues also cross-referenced the data to each creature's geographical location.<sup>2</sup> Nobody had done this before. To their great surprise, "animals grouped together by molecular trees lived more closely together geographically than the animals grouped using the morphological trees",<sup>2</sup> leading Prof Wills to admit:

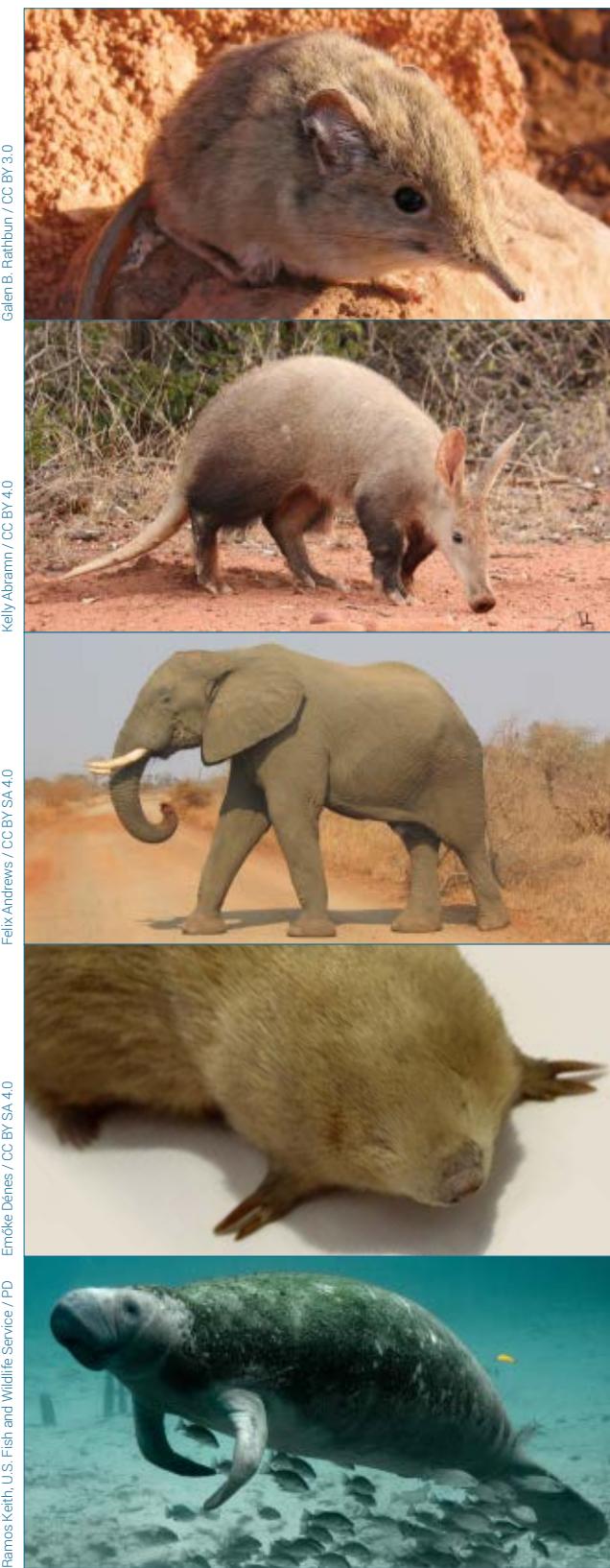
"... it turns out that we've got lots of our evolutionary trees wrong. For over a hundred years, we've been classifying organisms according to how they look and are put together anatomically, but molecular data often tells us a rather different story."<sup>1</sup>

Just how challenging this finding is for evolution should be obvious if you refer to the pictures of the very different members of the Afrotheria (figure 1), while reading the following:

"For example, tiny elephant shrews, aardvarks, elephants, golden moles and swimming manatees have all come from the same big branch of mammal evolution—despite the fact that they look completely different from one another (and live in very different ways).

Molecular trees have put them all together in a group called Afrotheria, so-called because they all come from the African continent."<sup>1</sup>

Think about that. The coded instructions of a creature's DNA are used to make all the proteins which comprise its anatomy. Supposedly, beneficial genetic mutations of this DNA are the raw material that natural selection works with, thereby driving the evolution of new tissues, organs, and body plans. If that is really the case, why the big disagreement between DNA/protein comparisons and the morphological comparisons (ones based on appearance)?



**Fig. 1.** From top to bottom: elephant shrew, aardvark, elephant, golden mole, and manatee

Galen B. Rathbun / CC BY 3.0

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Ramos Kent U.S. Fish and Wildlife Service / PD | Emidr Dénes / CC BY SA 4.0

Professor Wills re-emphasized this evolutionary dilemma more recently, once again highlighting his team's counterintuitive study findings:

"Evolutionary trees based on DNA data were two-thirds more likely to match with the location of the species compared with traditional evolution maps. In other words, previous trees showed several species were related based on appearance. Our research showed they were far less likely to live near each other compared to species linked by DNA data."<sup>5</sup>

In other words, such research upsets evolutionary family trees across the board. For a long time, Wills writes, similarities in the brains and skeletons of bats and primates (in which he includes humans) led evolutionists to believe they were close relatives. The molecular data has surprised them all: "Astonishingly, bats turn out to be more closely related to cows, horses and even rhinoceroses than they are to us."<sup>5</sup>

### "Do we need a new theory of evolution?"

Some evolutionary scientists have dissented from pure Darwinism for decades, giving rise to many alternative theories and models of evolutionary change (see Appendix). However, the neo-Darwinian version of evolution is still by far the most popular. It is still the version that school children learn and that is generally propagated by the mainstream media. Those students of evolution conversant with the trajectory of evolutionary thinking cannot avoid the conclusion that there is something amiss—the proliferation of alternative ideas and models is a big clue.

The entire edifice of evolution has been built upon supposedly similar appearances of organisms, both living and extinct. As we have already seen, the central Darwinian idea that similarity of appearance establishes relationship is being proven wrong. Fossil experts need to face the facts: in one fell swoop, the data from molecular biology is sweeping aside almost two centuries of palaeontological theorizing and popular storytelling. Living organisms frequently share more genetic similarity with very different-looking creatures in the same geographical location than with more morphologically similar ones in a different part of the world. This being the case, of what value are studies that focus on the minutiae of anatomical comparisons between long extinct creatures, most of them based upon very fragmentary remains, and sometimes on mere bony scraps?

However, it would be naïve to think that this conflict between theory and facts, stupendous though it really is, will cause a fundamental reassessment of the 'fact' of evolution itself. Far too much is at stake. There is much more to the origins debate than the factual data of biology, genetics, and palaeontology. For many, evolution is foundational to a worldview that has dispensed with the Creator God. 'True believers' have invested too much in the paradigm to question

its reality, not just intellectually, but also emotionally, even spiritually.

Refreshingly, however, more and more scientists *are* thinking outside the box. Contrary to the slur that they are all closet religious fundamentalists, many of these people have no overt faith commitments. Their concern is to go where the evidence leads. They wish to be unshackled by dogma and are prepared to stand in defiance of those who would restrict freedom of thought and speech in science—whether the intimidating priests of neo-Darwinism or their willing acolytes in the secular media.

For some years now, a growing list of doctoral scientists from academic institutions around the world have signed up to the following statement at the website, *A Scientific Dissent From Darwinism*:

“We are skeptical of claims for the ability of random mutation and natural selection to account for the complexity of life. Careful examination of the evidence for Darwinian theory should be encouraged.”

At the time of writing, this list exceeds 1,200 Ph.D. scientists, 38% of whom are department professors.<sup>6</sup> In spite of their impeccable credentials, critics have tried to write them off as scientific ignoramuses, guilty of muddying the waters over the supposedly clear and abundant evidence for evolution. However, such lame attempts to dismiss this large body of critics of neo-Darwinism have done nothing to shore up the inadequacies of a failing theory.

For some time, in fact, mainstream biological scientists *who believe in evolution* have been voicing their frustration about the lack of debate about the problems with the standard theory. Finally, it seems, some of these complaints are getting through. In June 2022, *The Guardian* (UK) even carried an article with the provocative title, “Do we need a new theory of evolution?” Writer Steve Buranyi pulled no punches:

“[There’s a problem with] the basic story of evolution, as recounted in countless textbooks and pop-science bestsellers. The problem, according to a growing number of scientists, is that it is absurdly crude and misleading.”<sup>7</sup>

For biblical creationists, exposés like this are encouraging. In spite of the very real conflicts between the facts and evolutionary theory, not to mention the many private disagreements among evolutionary scientists themselves, few have been willing to air these things publically. Not surprisingly, the average person has assumed all is well. A very telling admission is that a plethora of popular science books, as well as school textbooks, are guilty of “absurdly crude and misleading” evolutionary story telling. *Evolutionary scientists* themselves are saying this! Over 20 years ago, James Williams, a trainer of teachers at University of Sussex (UK) similarly bemoaned that “Examples of evolution used in textbooks are flawed and in need of radical updating” and

“Our teaching of evolution is poor”.<sup>8</sup> The situation is now much worse.

Buranyi did not stop there, however. Drastic problems with neo-Darwinism, the so-called ‘modern synthesis’, were recognized decades ago; i.e. the idea, long championed by the likes of Richard Dawkins, that natural selection sorts out and selects from random mutations. A new generation of evolutionists have long realized it is not the answer, as Buranyi explains:

“According to the modern synthesis, even if mutations turned out to be common, natural selection would, over time, still be the primary cause of change, preserving the useful mutations and junking the useless ones. But that isn’t what was happening. The genes were changing—that is, evolving—but natural selection wasn’t playing a part. Some genetic changes were being preserved for no reason apart from pure chance. Natural selection seemed to be asleep at the wheel.”<sup>7</sup>

It is true that genes may change, but none of these instances is of the slightest encouragement for neo-Darwinian evolution. Instead, mutations invariably disrupt and break things. Mutations can lead to new alleles, new versions of existing genes, leading to new *traits* (although many traits are not the result of mutations). However, mutations have *never* been observed to generate the sort of novel complexity that neo-Darwinists wish for. Moreover, evolutionists’ confidence in the power of natural selection to help generating functional new features has been misplaced.

Buranyi’s assessment is apt, but again reveals how few experts have the appetite to come clean about the abject failure of neo-Darwinism:

“Perhaps the biggest change from the theory’s mid-[20<sup>th</sup>] century glory days is that *its most ambitious claims*—that simply by understanding genes and natural selection, we can understand all life on earth—*have been dropped, or now come weighted with caveats and exceptions*. This shift has occurred with little fanfare. ... no formal reckoning with its failures or schisms has occurred [emphases added].”<sup>7</sup>

### **“Neo-Darwinism must mutate to survive”**

Two months after the *Guardian* article, U.S. co-authors and professors Olen R. Brown and David A. Hullender joined the fray with a paper titled, ‘Neo-Darwinism must mutate to survive’.<sup>9</sup> They are adamant that the small-scale changes *observed* in the natural world, often dubbed ‘microevolution’, are of absolutely no help in explaining the *imagined* large-scale changes purported by Charles Darwin and his successors. Coming at things from a different angle, Brown and Hullender highlight the fact that the *statistical improbability* of neo-Darwinism is in the order of  $10^{-50}$ ,

putting the theory's ability to account for genuinely novel complexity (macro changes) into the realm of the impossible:

"Thus, survival of the fittest is illogical when proposed as adequate for selecting the origination of all complex, major, new body-types and metabolic functions because the multiple changes in multiple genomes that are required have intermediate stages without advantage; selection would not reasonably occur, and disadvantage or death would logically prevail."<sup>9</sup>

This is yet another strike against the cherished theory, and this is seriously confronting for proponents of naturalism. What, then, is the alternative, if mutation and selection cannot produce significant evolutionary change? Could there be purpose in biology, 'Intelligent Design'? That, of course, has long been a big no-no for a majority of scientists. Consequently, it is refreshing to see Brown and Hullender saying that "Logic demands that it [evolution] be open to investigation. This first requires an openness to ideas and science must be open to new ideas."<sup>9</sup>

Moreover, while not using Michael Behe's famous phrase, Brown and Hullender acknowledge the serious challenge that 'irreducible complexity' poses for large-scale evolutionary change:

"Darwin wrote in *On the Origin of Species*... : 'If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down. But I can find out no such case.' Today, Darwin's missing cases are abundant including each complex transition to a new body type, metabolic cycle, or metabolic chain. Multi-step processes are routinely required at every evolutionary step."<sup>9</sup>

### **"Darwin got it wrong"**

One could be forgiven for thinking, from this recent flurry of high-profile admissions that all is not well with the theory of evolution, that these sorts of admissions are new. In fact, there have been murmurings for quite some time. For instance, in their book *What Darwin Got Wrong* (2011), Jerry Fodor and Massimo Piattelli-Palmarini say Darwinism is "fatally flawed", stating candidly:

"OK; so if Darwin got it wrong, what do you guys think is the mechanism of evolution?" Short answer: we don't know what the mechanism of evolution is. As far as we can make out, nobody knows exactly how phenotypes evolve."<sup>10</sup>

"In fact, we don't know very well how evolution works. Nor did Darwin and nor (as far as we can tell) does anybody else."<sup>11</sup>

The opinions of writers of their stature are not easily dismissed. Now retired, Fodor is a respected American philosopher whose career included long stints at Massachusetts Institute of Technology, City University of New York, and Rutgers University. Piattelli-Palmarini's career has taken in biophysics, molecular biology, and he is currently Professor of Linguistics and Cognitive Science at the University of Arizona. They can't be justly accused of having a proto-teleological bias of some sort. Rather, "we do want, ever so much, to be secular humanists. In fact, we both claim to be outright, card-carrying, signed-up, dyed-in-the-wool, no-holds-barred atheists. We therefore seek thoroughly naturalistic explanations of the facts of evolution."<sup>12</sup>

In the 2011 edition of *What Darwin Got Wrong* (first published in 2010), Fodor and Piattelli-Palmarini included an extra chapter, 'Afterword and reply to the critics', confiding that "the book was received very badly [by their evolutionary colleagues]. Almost (though not quite) all the reviews were hostile and some were hysterical."<sup>13</sup> Nevertheless, in the years that followed, more scientists have shown themselves willing to raise their heads above the parapet.

In 2013, Carrie Arnold, a science writer for *New Scientist*, showed unusual candour by emphasizing something that creationist biologists had been pointing out for a long time:

"While natural selection explains how species change over time, accounting for how new species arise in the first place has proved rather trickier. Darwin's *On the Origin of Species* actually said nothing at all about the origin of species."<sup>14</sup>

Had an advocate of biblical creation or intelligent design made the same point, one easily can imagine the accusations and cries of 'foul'. The same year, Stephen Meyer had this to say in his *tour de force* of a book, *Darwin's Doubt*:

"The technical literature in biology is now replete with world-class biologists *routinely expressing doubts* about various aspects of neo-Darwinian theory, and especially about its central tenet, namely, the alleged creative power of the natural selection and mutation mechanism [emphasis added]."<sup>15</sup>

Is it credible that scientists have been unable to flesh out the main claim of the title of Darwin's famous 1859 book, *On the Origin of Species*? After a further 160 years of research by a vast number of scientists? In 2015, biological science writer Bob Holmes admitted:

"Speciation still remains one of the biggest mysteries in evolutionary biology and the unexamined view of natural selection leading to large-scale innovations is not true."<sup>16</sup>

"Not true", notice. Darwin really did get it wrong! The same year, Suzan Mazur interviewed a number of world-leading biologists and published these exchanges in her book, *The Paradigm Shifters: Overthrowing the hegemony*

*of the culture of Darwin.* We will consider just two of these dissenters from neo-Darwinism.

Firstly, James A. Shapiro (University of Chicago) had this to say:

“Genome change is not the result of accidents. … It’s in the course of fixing damage or responding to other inputs … that cells turn on the systems they have for restructuring their genomes. So what we have is something different from accidents and mistakes as a source of genetic change. We have what I call ‘natural genetic engineering [emphasis added].’”<sup>17</sup>

In other words, this professor of biochemistry and molecular biology is adamant that random mutational change is of no help to evolution. Shapiro is another scientist not easily dismissed. As well as stellar academic achievements, he has been awarded an OBE.<sup>18</sup>

Secondly, the late Mae-Wan Ho (co-founder and director of *Institute of Science and Society*, UK) was an accomplished geneticist. She was blunt about the status quo as she saw it:

“I think the Modern Synthesis has got to be completely replaced, and unfortunately, those people who are very attached to neo-Darwinism won’t look at the evidence. A lot of them don’t know molecular genetics at all. Or like [Richard] Dawkins, they will say, I just don’t believe it. They’re not scientists.”<sup>19</sup>

These are just a few of the many voices of scientists, most of them evolutionists, who have been calling for an honest appraisal of the state of evolutionary theory. They strongly believe that a new theory of evolution is desperately needed.

### Wishful thinking is no answer

Many others, however, prefer to hide their heads in the sand, holding on to the irrational notion that evolutionary change surely *must* have occurred, in spite of these apparently insuperable scientific challenges. Maybe we are underestimating evolution’s ability?

“Perhaps evolutionary innovation is easier than we think? Perhaps evolution does not have to wait for innovations? Perhaps its creative engine is more powerful than we give it credit for? The astonishing speed with which evolution can respond to new opportunities suggests this possibility.

“… What if many innovations arise before their time, but flourish only when conditions are right? [emphases added].”<sup>20</sup>

To which we reply, there is no crime in using one’s imagination, but ‘perhaps’ and ‘what if’ are not acceptable substitutes for tried-and-tested scientific discoveries.

The real answer to the question posed by this article is ‘no, a new theory of evolution is not needed.’ Instead, evolutionists ought to stand back and ask themselves: ‘if neo-Darwinian evolution has been falsified (and Darwin

and his followers are wrong), why am I so driven to find an alternative *naturalistic* explanation for origins?’ What is wrong with acknowledging that living things show profound evidence of intelligent design, and indeed were designed to adapt? Why not follow the evidence where it leads?

### Appendix: The evolution of evolutionary theory

What follows is a chronological list of different evolutionary theories that the author has become aware of and studied since the late 1980s. It is not exhaustive; further theories are given at the end of these ten items:

1. *Darwinism* (1859, Charles Darwin). The standard view of natural selection, prior to the advent of genetics and of knowledge about genetic mutations.
2. *Social Darwinism* (a term first used in 1877, but more popular in the post WWII period). It has links with the early eugenics movement and is the attempted application of evolution to human sociology and politics.
3. *NeoDarwinism* (late 1930s, later dubbed ‘evolution by creeps’ by Gould, in response to those who criticised his and Niles Eldredge’s Punctuated Equilibrium model, see below). It is the result of the synthesis of classical Darwinism with genetics (the idea of mutations as the source of novelty). There have been numerous prominent advocates: Theodosius Dobzhansky, Ronald Fisher, John B.S. Haldane, Ernst Mayr, George Gaylord Simpson, and more. Richard Dawkins and Jerry Coyne are just two of today’s advocates. Sympatric and allopatric speciation are key ideas within this model.
4. *Hopeful Monster hypothesis* (1940, Richard Goldschmidt, his own term for his idea!). A kind of saltational evolutionary theory that involves large mutations in order to bridge the perceived gulf between micro- and macro-evolution.
5. *Punctuated Equilibrium* (1970s, dubbed ‘evolution by jerks’ by its critics), including allopatric speciation as a central idea. Key advocates: Stephen Jay Gould and Niles Eldredge.
6. *Symbiogenesis* (an old term, from 1926). It was made into a full-blown evolutionary theory by Lynn Margulis (1938–2011) while she was a post-doctoral scientist, but especially following her books in 1998 and 2002. She became well known from the early 1970s after publishing her *endosymbiosis* theory to explain the origin of mitochondria and chloroplasts from mergers of various prokaryotic organisms.
7. *Neutral Theory* (1960s). The key advocate was Motoo Kimura (Japanese; mentioned in John Sanford’s book, *Genetic Entropy & the Mystery of the Genome*); see also Kimura’s influential 1983 C.U. Press book, *The Neutral Theory of Molecular Evolution*.

8. *Evo-Devo* (or evolutionary development). It is not easy to give a date as this includes many ideas and discoveries stretching back a century. Since the 1980s, the discovery and subsequent elucidation of the function of Hox (homeotic, homeobox) genes has been a key part of *Evo-Devo*. In the thinking of many biologists, it is now a strong contributory factor to large-scale evolutionary change. Well known advocates are Sean B. Carroll and Jack Horner.
  9. *Natural Genetic Engineering* (2011 book, *Evolution: A view from the 21<sup>st</sup> Century*, James Shapiro); a second edition appeared in 2022. To borrow from one of the chapter titles of the book, it is a ‘systems approach to generating functional novelty’. James Shapiro explicitly denies that random mutation and natural selection are capable of large scale evolutionary change; e.g. “The role of selection is to eliminate evolutionary novelties that prove to be non-functional and interfere with adaptive needs. Selection operates as a purifying but not creative force [emphasis added].”<sup>21</sup>
  10. *Complexity by Subtraction* (a 2013 paper in *Evolutionary Biology*<sup>22</sup>) is an attempt to get round the challenges of irreducible complexity (Michael Behe). Proponents: Daniel McShea and Wim Hordijk.
- In addition, Andrew Lamb has helpfully listed the following online:

“Other (mostly discarded) theories of evolution include Maximum Entropy Production (MEP), Population Dynamics, Facilitated Variation, Semi-Meiosis, Niche Construction, Panspermia, Metabolic Rate Theory, Zoogenesis, Lamarckism, Orthogenesis, Pangenesis, Gaia Theory, Evo-Devo, Symbiogenesis. There are many more.”<sup>23</sup>

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# Enantiomeric amplification of L- amino acids: part 4—based on subliming valine

Royal Truman

In laboratory experiments, sublates of valine (Val) and isoleucine (Ileu) formed conglomerate crystals enriched in the L-enantiomer if a sizeable initial excess of L was used in the experiment. L excesses of these two amino acids (AAs) were also able to enrich a racemic leucine (Leu) mixture, whereas Leu alone sublimes to form only racemic crystals. The conditions necessary for these enrichments could not have plausibly occurred naturally. Thoroughly homogenized, pure AAs had to be placed rapidly at the bottom of a previously heated flask set to 430°C, which is more than 130°C above their decomposition point. This caused the AAs to sublime instantly and then equilibrate rapidly on a much cooler two-dimensional surface before too much decomposition occurred. The abnormally high sublimate concentrations produced unique L-L interactions and a spatial gradient of L/D proportions. Increasing the L/D ratio would require repeating this process many times using only nearby sublimate portions having more L. Instantaneous transfers from a low-temperature location to avoid decomposition to a location hotter than 100°C will not occur naturally. Instead, any sublimate surviving degradation would remix and combine with racemic AAs in the environment. Worse, amino acids surviving the intense heat would have suffered a *decrease* in original enantiomeric excess.

I continue here the series dealing with proposals on how a small excess of an amino acid (AA) enantiomer might be amplified under natural conditions. The L-enantiomers of nineteen biogenetic AAs are coded for by the genetic code and used to construct proteins. The source of pure L-enantiomers in the absence of pre-existing enzymes, themselves built from only L-AAs, has been an enduring source of discomfort for evolutionists. This discomfort implies that the origin of cells involved more than natural chemical processes.

## Sublimation of valine at very high temperature

Viedma and colleagues reported that when an equal proportion of D- and L-enantiomer of valine (Val) is rapidly sublimed at 430°C, the condensate on the wall of the glass vessel forms racemic conglomerates (i.e. pure D- and L-enantiomers crystallize into different crystals which are mixed together).<sup>1</sup>

Obtaining *conglomerate crystals* was noteworthy since Val, like almost all proteinogenic AAs, forms *racemic crystals* under milder conditions (i.e. the D- and L-enantiomers are intimately mixed in the same proportion within the same crystal).<sup>2</sup> The observed switch from an initial heated racemic mixture to a conglomerate was studied using Powder X-ray (PXR) diffraction.

Very specific laboratory conditions were necessary to obtain this effect.<sup>1</sup> A hotplate stirrer was set to 430°C, and a 1000-mL flask placed on top for 3 mins, creating an optimal temperature gradient. A Val mixture having 40% e.e.<sub>L</sub> (*enantiomeric excess* of L) was then placed on the bottom of the flask and stirred

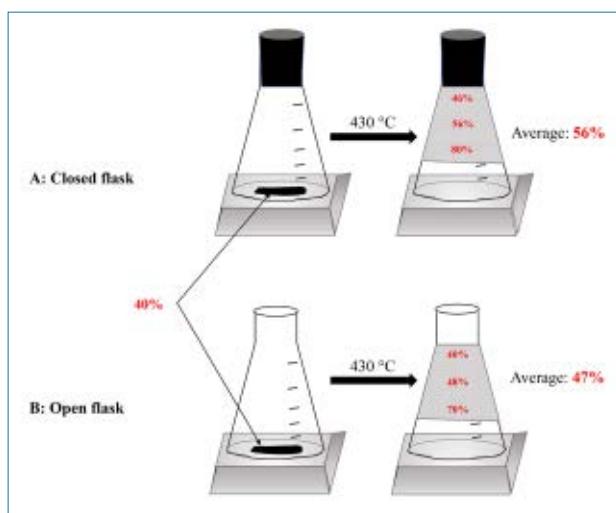
for a few seconds to maximize contact with the hot surface. Sublimation occurred almost instantly, and a dense cloud of condensing microcrystals was seen for ~2 mins on the much colder higher levels of the flask.

Chiral HPLC (High Pressure Liquid Chromatography) analysis did not reveal any enantioenrichment in the initial deposit, but the enantiomeric enrichment of the sublimate continued to ascend for about 10 mins. After completion, the system was cooled to room temperature. When using a closed flask (see figure 1A), a gradual vertical separation of Val enantiomers was found. The e.e.<sub>L</sub> ranged between 46%, at the top, to 80%, at the bottom, for an average of 56%. The experiment was repeated using an open flask, leading to lower e.e.<sub>L</sub> values having an average e.e.<sub>L</sub> of 47% (see figure 1B).<sup>1</sup> The latter represents a net increase of 7% in e.e. since the initial e.e.<sub>L</sub> was already 40%.

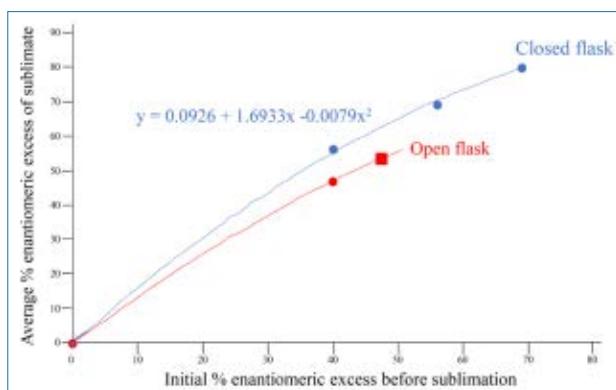
The authors did not know the cause for this spatial enantiomer separation. One possibility is that, analogous to attrition-enhanced deracemizations, tiny crystal fragments with more L members may have interacted favourably in the sublimate, thereby offering a greater surface area for further growth.<sup>1</sup>

As mentioned above, starting with a 40% e.e.<sub>L</sub> Val sample, the sublimate had an average e.e.<sub>L</sub> of 56% using a closed flask. When the sublimed crystalline material was isolated and used for a second sublimation experiment, the new crystals had an average of 69% e.e. Repeating a third time led to a further improvement, with sublimate now having an average of about 80% e.e.<sup>3</sup>

We can use these three data pairs for the closed-system experiments and assume that an initial 0% e.e. would produce



**Figure 1.** Gradient-like separation of 40% L-enantiomer excesses of valine sublimed at 430°C. A: Closed flask, B: Open flask.<sup>1</sup> (Author's own artwork based on a figure from ref. 1.)



**Figure 2.** Empirical relationship between initial % e.e. L-valine and average % e.e.<sub>L</sub> of the sublimate.<sup>1,3</sup> Blue: using data from closed-flask experiments. Red: estimated trend using an open flask. The red square was calculated; see main text.

a sublimate having 0% e.e. to construct an empirical first-order polynomial curve. This will allow calculating the results for other initial values of e.e.<sub>L</sub> (see figure 2, blue line).

Repeated cycles to amplify the e.e.<sub>L</sub> were not reported in the *open system*. This is the environment which would occur naturally.<sup>4</sup> A single data point is available from the open flask experiment which also started with 40% e.e.<sub>L</sub>, which produced a sublimate having an e.e.<sub>L</sub> of 47%.<sup>1</sup> Beginning a new sublimating cycle with 47% (instead of 56% as before), and using the empirical equation shown in figure 2 derived for the closed flask predicts an e.e.<sub>L</sub> of 62%:

$$\text{e.e.}_L = 0.0926 + 1.6933 \times (47) - 0.0079 \times (47)^2 = 62$$

However, starting with 40% e.e.<sub>L</sub> led to 9% (56% – 47%) less enhancement in the closed flask than the open flask

experiment, so we subtract 62% – 9% = 53%, shown as a red square in figure 2. Since the curve for closed flask behaviour increases less rapidly (see figure 2) the correction should be even more than 9%.

Remarkably, in his attempt to find a way to amplify an initial e.e., Viedma has documented an effective manner to *decrease* the initial e.e. throughout nature! From figure 1B, for the open flask experiments we see that near the intense heat source the e.e.<sub>L</sub> was 70%, and towards the top it was down to exactly the starting value of 40%. Since mathematically the total amount of L + D-AA is constant (or lower if racemization occurred at such high temperatures) and all the AA sublimed, then beyond the 40% layer the rest of the AA must have an e.e.<sub>L</sub> < 40%!

Furthermore, the process of freezing sublimate in nature would have been spread out over far greater distances than a few centimetres as in the cold flask. Therefore, there would have been a continuum of e.e.<sub>L</sub> values whereby the material closest to heat sources hundreds of degrees C would have been preferentially thermally destroyed. The surviving AA could only average to a lower e.e.<sub>L</sub> than initially present. Future cycles would have continually been enriched in the ‘wrong’, i.e. D-enantiomer.

### Using sublimed amino acid mixtures at very high temperature

Further experiments were reported by Viedma *et al.* using the hot stirring plate set to 430°C and a 1000-mL flask setup.<sup>3,5</sup>

Experiments were conducted using four AAs which were known to crystallize from aqueous solutions as racemic compounds (i.e. the D- and L-enantiomers are mixed in equal proportions within the same crystal). Viedma *et al.* discovered that Val and Ileu recrystallized after sublimation into conglomerates (i.e. the individual crystals were composed of pure D- or L-enantiomers), whereas leucine and alanine recrystallized as usual into racemic compounds, as shown in figure 3.<sup>3</sup>

Since enantiomeric separation via sublimation requires an AA to crystallize as a conglomerate, the researchers decided to combine an AA which conglomerated with one which did not. The results of sublimation experiments at 430°C conducted in *closed flasks* are shown in table 1.

A mixture of 40% e.e.<sub>L</sub> Val with 40% Leu led to a sublimate containing 51% e.e. Leu, see the first row in table 1.

The results using racemic Ala instead of racemic Leu were disappointing. The authors wrote:

“Alanine (the simplest chiral amino acid) was quite reluctant to undergo this sort of resolution, either with valine or isoleucine, and a poor increase in ee (ca. 4% on average) could be measured in the presence of scalemic isoleucine.”

This is the last row shown in table 1. The results of mixing 40% e.e.<sub>L</sub> Val with 40% Ala were not reported.

Note that experiments using Val and Ala were also conducted, but why were the exact values not reported? Also, an estimate of experimental reproducibility would have been helpful instead of only reporting an average value. No mention was made in the paper nor the Electronic Supplementary Information about experiments being repeated, so what was the basis for choosing which results went into the *on average* of ca. 4% when Ileu was used instead of Val? Considerable experimental error can be surmised, since derivatization of the AAs using thiol isobutyryl-L-cysteine and o-phthalaldehyde followed by rehydration were carried out to facilitate the HPLC analysis.<sup>3</sup> Therefore, one should conclude provisionally that amplification was demonstrated for only one AA (Leu), but for Ala this is doubtful.

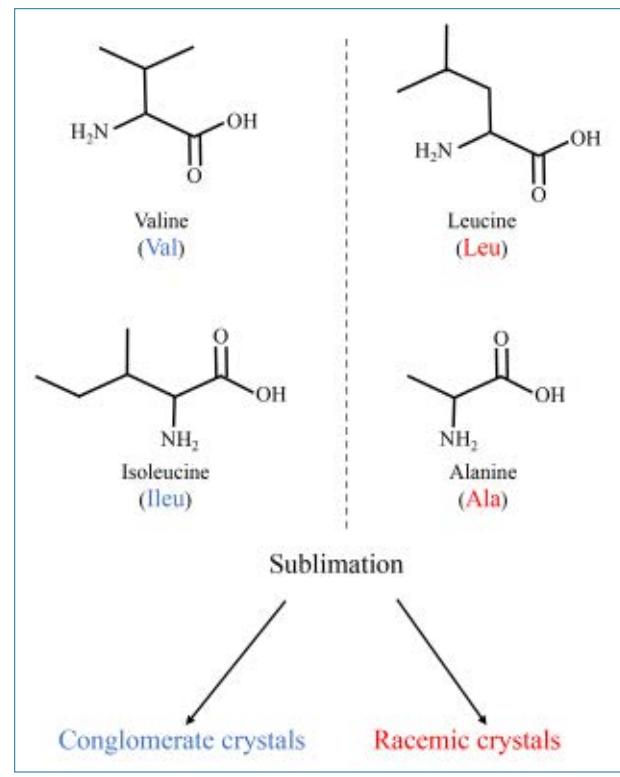
Thus, amplification was achieved for one biological AA, Leu, which doesn't form conglomerates. This was achieved by both Val and Ileu; see the data in table 1. Interestingly, the trend in amplification contradicted what Tarasevych *et al.* found, namely that partial sublimation of L-asparagine with various racemic AAs led to a sublimate enriched with the *D-enantiomer* (discussed in Part 6 of this series)!<sup>6</sup> Whereas Viedma *et al.* would argue for the *sublimate* being a source of L enrichment, Tarasevych *et al.* would have to use the *residue* for this purpose. Whatever the phase selected, some mixtures of AAs might have *increased* the e.e.<sub>L</sub> of some AAs but concurrently *decreased* the e.e.<sub>L</sub> of other AAs.

The authors were not sure what the basis for these effects was. In the case of Val and Ileu crystals, the sublimate might be deposited on pre-existing crystals, moving upwards, away from the heat source. The experimental observation was that the highest e.e. was produced at the front sublimation line and decreased gradually upwards further from the intense heat source, the same effect reported above in figure 1.

### High temperature diffusion would decrease enantiomeric excess

As mentioned before, no e.e. was found in the initial deposit, but this developed over about 10 mins as the sublimate continued to ascend the inner flask surface. The much cooler outer flask surface served to artificially concentrate the sublimate. We can make some very rough calculations to illustrate this.

From experience, we know that if a gas like HCl is released we will soon smell it a long distance away. We can envision a large open natural hot setting with a thermal gradient maximizing at the bottom at ~430°C into which an AA is suddenly placed. Some of the hot gaseous AA would soon diffuse, say one to 10 metres, representing a volume  $\approx 10^6\text{--}10^9\text{ cm}^3$ . We don't know the thickness of sublimate formed on the flask surface in the experiments, but based on the minuscule size of the AAs involved let us assume this would be  $<0.01\text{ cm}$ , spread over a glass surface of  $\sim 10^2\text{ cm}^2$ . This would imply that the sublimate had been compacted into an effective volume of



**Figure 3.** Racemic crystals of valine and isoleucine sublime and then recrystallize as conglomerate crystals. Racemic crystals of leucine and alanine sublime and then recrystallize as racemic crystals.<sup>3</sup>

$<1\text{ cm}^3$ , i.e. by a factor of millions to billions. Furthermore, the concentration of AA and e.e.<sub>L</sub> used were considerably higher than naturally plausible. Clearly, the laboratory conditions had artificially facilitated L-L and L-D equilibration interactions. To further amplify this, the authors manually dissolved the sublimate from the surface, benefitting strongly from the highest e.e. obtained, which was just a few centimetres from the heat source. Figure 1 shows how rapidly e.e. decreased with distance, and sublimate located one to ten metres away would almost certainly be racemic. Therefore, the e.e.<sub>L</sub> values shown in figure 2 are not representative of what would occur under natural conditions.

We can use the red curve in figure 2 for the open flask and assume Val is initiated with a very generous e.e.<sub>L</sub> of 10% instead of the completely unrealistic 40%. Of course, the flask surface would still constrain the volume since sublimate can only escape from the distant narrow opening after being exposed to the cooler glass surface.

Even retaining all the unrealistic optimizations used by the researchers for the open-flask experiment (red curve in figure 2), the e.e.<sub>L</sub> of the sublimate would only increase by about 2%, while simultaneously lowering the e.e.<sub>L</sub> in the residue left behind. But flash sublimation would be a rare event, and, realistically, most of the sample containing an initial assumed 10% L excess would have thermally decomposed before being exposed to a temperature near 430°C.<sup>8</sup>

**Table 1.** Enantiomer enrichments resulting from mixtures of amino acids. Enantiomeric excesses of sublimates were determined by chiral HPLC and represent average values in the entire sublimate.<sup>3</sup>

Initial amino acid mixture (% ee)	Resulting sublimed material (% ee)
L 40% Val + L 40% Leu	L 54% Val + L 51% Leu
D 40% Val + D 40% Leu	D 52% Val + D 50% Leu
L 40% Ileu + L 40% Leu	L 54% Ileu + L 64% Leu
L 40% Val + L 40% Ileu	L 57% Val + L 57% Ileu
L 57% Val + L 57% Ileu	L 68% Val + L 69% Ileu
L 40% Ileu + L 40% Ala	L 55% Ileu + L 44% Ala

It is instructive to recall from figure 1B that only a few centimetres from the heat source the sublimate e.e.<sub>L</sub> was 40%, exactly the same as the initial excess. Zero enrichment was now present.

Without deliberate researcher intervention, the true net overall effect of this scenario would be to decrease any local e.e.<sub>L</sub> initially present in nature. Repeating the cycles through renewed exposure to very high temperatures would ensure that the original e.e.<sub>L</sub> would eventually be destroyed. There is no reason why nearly pure L sublimates would never again be subjected to the high temperatures.

### Summary critiques of these studies

There are several objections to using these results to claim amplification of L-AAs would have occurred under prebiotic conditions.

- The results relied on preferential L-L vs L-D interactions, which required very concentrated AAs to have a measurable effect. Finding 0.05 gm of pure AA sublimate on a few cm<sup>2</sup> of surface by chance is unrealistic by many orders of magnitude.<sup>1</sup> Under natural conditions, sublimed AAs would be significantly diluted by other substances and probably often be bound in large chemical complexes (as observed in meteorites).<sup>7</sup> An initial e.e.<sub>L</sub> of 40% is considerably higher than anyone has claimed could have formed naturally. These two factors alone suggest that the necessary inter-AA interactions would not naturally occur to a detectable level. Val has a decomposition point of 295–300°C.<sup>8</sup> In an important report, Weiss *et al.* monitored the thermal decomposition of all 20 proteinogenic AAs, using calorimetry, thermogravimetry, and mass spectrometry. For the 8 AAs for which they reported in detail, the decomposition temperatures ranged from 185 to 280°C, with an average of 235°C. They concluded that the decomposition analyses

“... put constraints on hypotheses of the origin, state and stability of amino acids in the range between 200°C and 300°C.”<sup>9</sup>

Viedma *et al.*'s results required all the AAs to be present and sublime quickly at ~430°C, more than 100°C above their decomposition point! These AAs would have been destroyed instead of being highly concentrated in a natural setting at such temperatures. Therefore, the researchers had to manually transfer the AAs from room temperature to the bottom of a preheated flask at 430°C within seconds. They also provided a much cooler, smooth, clean glass surface only a few centimetres away to capture the sublimate. Only through such manipulations was the destruction of the AAs avoided.

Besides decomposing, all AAs would sublime in free nature as soon as a sufficiently high temperature was reached, thereby rapidly dissipating over time. Without a high density of AA having a large e.e.<sub>L</sub>, the requisite L-L interactions would have been absent.

- As pointed out above, beyond some distance from where sublimation had initiated the e.e.<sub>L</sub> would have been *lower* than the initial value. The portion with highest e.e.<sub>L</sub> would have been located nearest the fierce heat source, and been the portion preferentially destroyed. Viedma's experiments have revealed an effective way to *decrease an initial e.e.<sub>L</sub> throughout nature!*
- There would have been no plausible terrestrial environment which satisfies all the prerequisites after the putative Late Heavy Bombardment is supposed to have racemized any surviving AAs.<sup>10</sup> Perhaps AAs could have been dissolved in hydrothermal vents, and some became isolated in a crevasse and desiccated. However, Sato *et al.* showed that AAs are destroyed under hydrothermal conditions. They experimented at 20 MPa pressure and all the AAs they examined decomposed at under 300°C.<sup>11</sup>

Viedma *et al.* alluded to sublimation in environments such as frozen planets with low or no atmospheric pressure.<sup>3</sup> This is not credible for many reasons:

- » Frozen planets don't provide high concentrations of AAs at temperatures ~430°C.
- » If AAs were located at such a temperature, they would not then be conveniently cooled about 200°C within seconds after sublimation to avoid obliteration.
- » Recycling frozen enriched AA back into an environment hundreds of degrees hotter without being destroyed for additional amplification cycles is not plausible.
- » These frozen planets would not be closed systems, so an excess of L-enantiomer would have dissipated slowly over millions of years at low temperatures and pressures instead of equilibrating on top of microcrystals.
- » Concentrations of L-L interactions at any location would have been very low.
- If a suitable environment had existed on Earth, temperatures ~430°C would have heated any water nearby, in which AAs would eventually find themselves, ensuring loss of any e.e.<sub>L</sub> through enantiomer racemization. Considerable loss of e.e.<sub>L</sub> would be very fast in aqueous solutions near the boiling point of water, on the timescale of mere hours or days.<sup>12</sup>

- Racemization would be faster the higher the e.e.<sub>L</sub> attained, since the back reaction L → D would be favoured by the higher concentration of L-enantiomer. Repeating the sublimation cycles of transferring cooled crystals back to a new very hot, dry surface somewhere by chance would require much time, during which racemization would occur. The higher the starting e.e., the more difficult to further enrich it.
- Beginning with an e.e.<sub>L</sub> on the order of 40% with all the optimized parameters used for the two AAs able to form conglomerate crystals will not occur naturally.
  - » Many parameters were optimized to shorten the exposure time to the intense heat and inevitable decomposition.
    - L- and D-enantiomers were ground in a mortar to increase their effective surface and to homogenize them to facilitate L-L interactions.
    - The AA mixture was stirred to ensure maximum contact with the hot plate and to maximize the number of L-L interactions.
    - The hot plate stirrer was previously heated so that sublimation was almost instant.
    - A cool surface was provided mere centimetres from where sublimation occurred.
    - The flask was prewarmed for 3 mins at 430°C to generate an appropriate thermal gradient.
    - The solid AAs were rapidly transferred manually from room temperature to the bottom of the hot flask.
  - » A high concentration of AAs will not penetrate a *closed container* which also happens to be over a hundred degrees above their decomposition temperature.
  - » Only an *open system* or a huge, closed volume is plausible as a natural environment, considering also that an e.e.<sub>L</sub> must subsequently become available for further chemical processing, such as forming peptides. But in this environment, highly concentrated sublimates will not form or equilibrate; instead, they will dissipate as soon as formed.
- The highest enrichment was produced in the sublimate closest to the heat source, where thermal decomposition was most likely to occur. In addition, this portion of the sublimate would be proximate to the remaining residue which had just preferentially lost L-enantiomer. Future remixing, especially with the help of moisture, would preferentially combine the most enriched L sublimate with the D-enriched residue, decreasing or even reverting the average e.e.<sub>L</sub>. Without this contribution from the most L-enriched AA, the remaining sublimate in an open system would have very little or no L excess; see figure 1B.
- Very few biogenic AAs form conglomerate sublimates, and only a single credible example of enrichment through mixing was reported, for Leu. This sublimation scenario cannot explain the source of the wide variety of L-AAs needed to form proteins. The results of sublimation experiments under vacuum pressures and lower temperature reported by

Tarasevych *et al.* need to be taken into account. Combining L-asparagine with several racemic AAs led to the *opposite effect*, namely a sublimate enriched with the D-enantiomer.<sup>15</sup> This illustrates how multiple random effects tend to maximize entropy, in this case racemization of amino acids.

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2. Valine was chosen for this study since this proteinogenic amino acid was found to have a slight excess of L-enantiomer in meteoritic samples.<sup>2</sup>
3. Viedma, C., Ortiz, J.E., de Torres, T., and Cintas, P., [Enantioenrichment in sublimed amino acid mixtures](#), *Chem. Commun.* **48**(30):3623–3625, 2012 | doi:10.1039/c2cc18129k.
4. A large number of AAs would not penetrate a closed environment. Besides, if multiple sublimation and cooling cycles could have occurred, the e.e. would have remained sealed in the closed environment. It would have racemized over deep time and would have been unavailable to undergo complex chemical reactions necessary for origin of life models.
5. 430°C was indeed used, and Viedma *et al.* did not mean 430K. Amino acids decompose at defined temperatures between 185°C and 280°C, so subliming at 430°C seemed unnecessarily hot.<sup>7</sup> Initially, it seemed that 430K might have been meant, since according to Glavin and Bada, “Amino acids have appreciable vapor pressures above 150°C and will sublime under partial vacuum at elevated temperatures without any racemization or decomposition.” (Glavin, D.P. and Bada, J.L., [Isolation of amino acids from natural samples using sublimation](#), *Anal. Chem.* **70**(15):3119–3122, 1998 | doi:10.1021/ac9803784.) 430K corresponds to 157°C. However, in multiple papers by Viedma *et al.* they refer explicitly to the use of 430°C.
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# Enantiomeric amplification of L-amino acids: part 5—sublimation based on serine octamers

Royal Truman and Stephen Grocott

The source of pure L-enantiomer amino acids (AAs) is a perennial problem for origin of life researchers. The experiments critiqued here claimed that a small initial enantiomeric excess of L-serine ( $e.e._L$ ) could be concentrated. L-serine is unique, being able to form octamer crystals from its sublimate. The octamer clusters which formed at lower temperatures were racemic, whereas at higher temperatures centred around 205°C a new kind of homochiral cluster formed. However, since serine rapidly racemizes and decomposes thermally, special experimental protocols were necessary, such as: premixing enantiomers; using an  $N_2$  gas flow to remove sublimate from the heat source; short heating times; and rapid freezing at a temperature hundreds of degrees Celsius lower than the heat source. These were not natural conditions. Critically, starting with a high  $e.e.$  produced a sublimate having lower  $e.e.$ . Worse, the net effect after prolonged heating was destruction of any initial excess for all AAs tested.

This is part 5 of a series dealing with proposals on how a small enantiomer excess of L ( $e.e._L$ ) amino acid (AA) might have been amplified in a putative prebiotic earth. Here We'll discuss some experiments involving serine octamers, which are often referred to in the evolutionary literature.

## Sublimation of serine at high temperature using zone refining

Klussmann *et al.* showed that some AAs can undergo enantiomeric amplification due to their equilibrium behaviour at the solid–liquid phase, with serine showing the largest effect.<sup>1</sup> This topic will be discussed in Part 8. Serine is unusual among the smaller AAs in that it has four functional groups able to form hydrogen bonds. This can lead to a much higher concentration of clusters upon sublimation, involving 2–8 serine molecules.<sup>2</sup> Serine octamer ions can form, and there is also evidence that neutral serine octamers ( $Ser_8$ ) form, but such clustering does not occur for the other DNA-coding amino acids, except to a very small extent by threonine and proline.<sup>3</sup>

Following up on these insights, Perry *et al.* decided to see if an initial serine  $e.e.$  could be amplified, using purification by an established method for solids called ‘zone refining’.<sup>3</sup> The experimental setup is shown in figure 1. About 100 mg of serine D, L mixture with a predetermined  $e.e._L$  was prepared and placed 3 cm from the end of a 22-cm Pyrex glass tube having an inner diameter of 16 mm. Enough acetone was added to make a paste, and a spatula was used to spread it along 11 mm of the inner surface while rotating the tube. The

end coated with Ser was attached to two Vigreux columns, each 13 cm long, and a glass tube 11 cm long was attached to the other end. The Vigreux columns part of the end glass tube was surrounded by a Styrofoam container full of dry ice.  $N_2$  gas was pumped continually at 45 cm<sup>3</sup>/mins from the coated end through the apparatus.

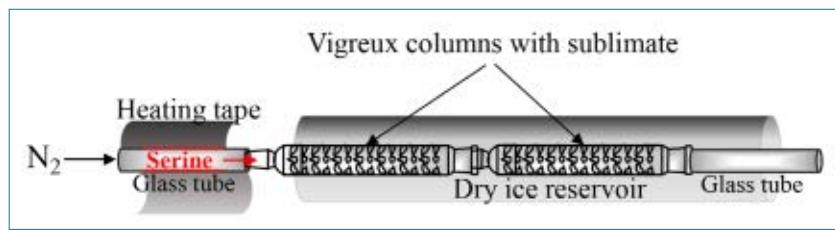
A heating tape about twice the width of the coated region was placed over it and then the temperature was slowly increased from room temperature to the experimental setting and held constant.

Degradation thermolysis products, including D,L-alanine, dehydroserine, and ethanolamine were obtained in high concentration (see figure 2).

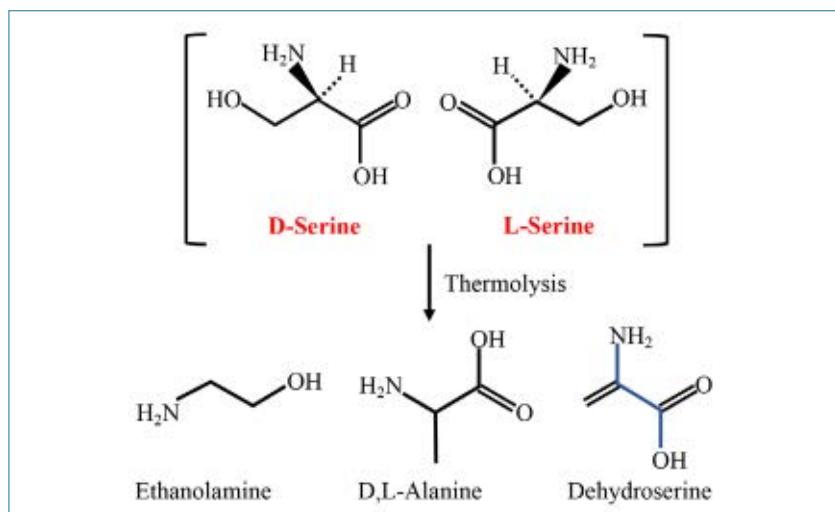
Alanine and ethanolamine made up 18% and 34% of the sublimate when heating 205°C after only 2 hours (h), and with increasing temperature this proportion increased as shown by the red line in figure 3.<sup>3</sup> Concurrently, the  $e.e._L$  of the sublimate serine decreased with temperature; see the blue line.

Figure 3 shows that at 205°C, where the highest  $e.e._L$  was obtained, about 60% of the serine was destroyed *after only 2 h of heating*. Importantly, heat caused rapid loss of L-enantiomer excess in the residue. In the words of Perry *et al.*:<sup>3</sup>

“The effect of racemization is even more clearly observed in the residue at higher  $e.e.$  values of L-Ser. When a 98%  $e.e.$  L-Ser sample is heated for 2 h at temperatures ranging from 175–250 °C in 15°C increments, the chiral purity of the residue decreases to 79% at 205 °C and to 45% at 250°C.”



**Figure 1.** Apparatus (not to scale) used to sublime serine and collect the sublimate.<sup>3</sup>



**Figure 2.** Thermolysis products of serine identified at 170°C and higher temperatures.<sup>3</sup>  
Source of figure: redrawn from ref. (3).

To emphasize, the experiment revealed a drop from e.e.<sub>L</sub> = 98% to 79% in only 2 h.

Another experiment revealed the same principle. When the residue of an initial 3% e.e. L-Ser sample was heated during the interval of 3–4 h the ~1 % sublimate produced had an e.e.L of 68%. However, the sublimate obtained during the heating period between 4–6 h dropped to 53%. This was attributed to racemization in the residue during the heating period.

The dramatic decrease in e.e.<sub>L</sub> with time in the heated region could not fail but have an effect on the e.e.<sub>L</sub> of the sublimate. In the temperature range of 190–210°C (which produced the highest amplification results), starting with 99% e.e.<sub>L</sub> serine led to a sublimate with an e.e.<sub>L</sub> of 74% after only 2 h of heating. This decrease was attributed to racemization via the thermolysis product dehydroserine.<sup>3</sup>

The rapid loss of e.e. explains why the N<sub>2</sub> flow was necessary: to decrease the time the sublimate would be exposed to high temperatures. These temperatures both racemized the serine and decomposed it.

A variant set of experiments confirmed the dependency of e.e. on temperature. A syringe pump was used to push the heating tape along the tube for ~18 h. Each experiment

started with 5% e.e.<sub>L</sub> serine, and figure 4 shows that the highest e.e. found (~65%) occurred at 205°C, with significantly lower values at slightly higher and lower temperatures.

The authors believe that enantioselective sublimation of serine occurred by forming homochiral octamers, a phenomenon displayed almost only by serine among the biological AAs. For the next best alternative, solid threonine with an initial 7% e.e.<sub>L</sub> at 208°C produced a sublimate having the much lower e.e.<sub>L</sub> of 1.2%.<sup>3</sup>

### Critique of these studies

The experimental conditions are not expected to exist naturally in a theoretical prebiotic setting. Perry *et al.* claimed:<sup>3</sup>

“The combination of chiral enrichment and physical separation (transport of the purified enantiomer), if it occurs repeatedly in a region with a modest temperature gradient, can readily be imagined to be a source of chirally pure serine.”

To be ‘readily imagined’ is no substitute for plausibility. A surface would have had to be densely coated with serine and with an excess of L-enantiomer. This would later be exposed to random blasts of heat at sublimating temperatures, like from a volcano. This does not produce an ideal smooth gradient, but would expose the serine to long and varying temperature fluctuations. Definitely not for only a few hours.

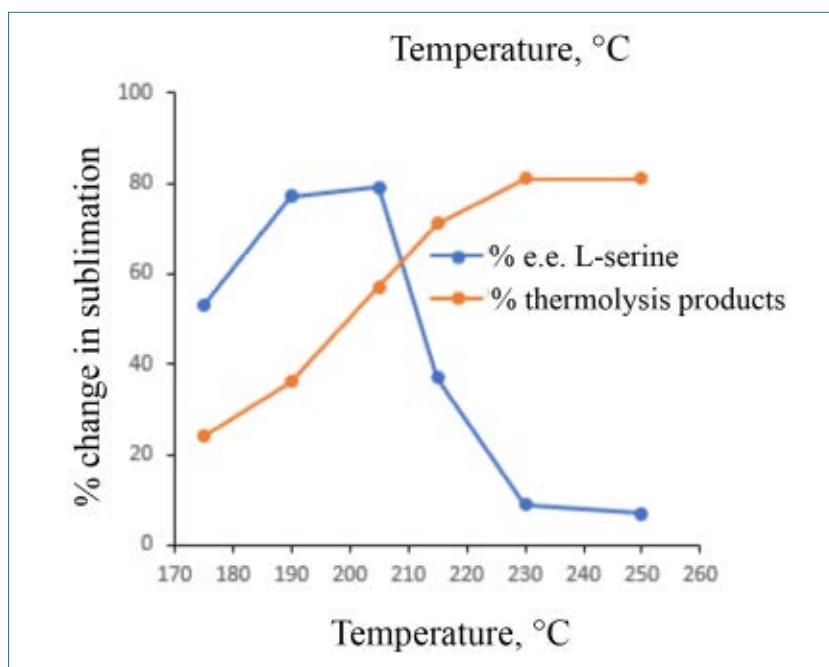
Here are some points to consider.

- The enantiomeric enrichment applied only to the AA serine. At the high temperature needed, all other AAs nearby would have racemized rapidly, especially if even a small amount of moisture was present.<sup>4</sup>
- The zone refining experiments were optimized after much preceding experimentation. To illustrate
  - » Direct exposure to the necessary high temperature was minimized by pumping N<sub>2</sub> through the apparatus, and dry ice was used to rapidly freeze the sublimate.
  - » Exposure to heat was usually limited to 2 h in one set of experiments and 18 h in another set. This was only long enough for 100 mg to produce about 1 mg sublimate.
  - » Vigreux columns were used to optimize enantiomer separation.

- Enantiomer enrichment was negligible—only  $\pm 20^\circ\text{C}$  from the optimal temperature of  $205^\circ\text{C}$ .
- Serine was destroyed and e.e. was negligible if serine continued to be exposed to the optimal temperature for just a few hours. An analogous natural setting would merely provide the ideal means of destroying existing serine, and especially any temporary e.e., after a few days.
- The maximum e.e.<sub>L</sub> achieved was much too low for biological purposes and was obtained for only serine.<sup>5</sup>
- The starting point was unrealistic. Any serine available would have degraded and lost any e.e. instead of waiting to be heated suddenly to  $\sim 205^\circ\text{C}$ . Therefore, the researchers began each experiment by placing pure serine on a pristine glass surface at room temperature, then rapidly heated it on the timescale of minutes to the final temperature.
- The enrichment obtained relied on preferential L-L, D-D, and/or L-D molecular interactions. This required a very high concentration of serine in the sublimate, which was achieved by deliberate laboratory manipulations (this would not occur naturally).
  - Instead of pure Ser, many other substances would have diluted the concentration, including other AAs.
  - Solid enantiomers were made as homogeneous as possible by grinding with a mortar and pestle, mixing with a spatula, and dissolving in acetone.
  - The entire Ser sample was heated at the same time, ensuring an enormous amount of sublimate would form during a short time interval.
  - The volume was severely constrained with a clean, smooth glass surface only centimetres away, at hundreds of degrees lower temperature, to trap the sublimate formed.

### Formation of homochiral serine octamers using a soldering gun

Electrospray ionization has been used with serine to form stable clusters of eight serine molecules under special conditions.<sup>6-8</sup> The latest reports showed that these octamers were formed by rapid sublimation.<sup>2,8</sup> Yang *et al.* achieved this in a series of experiments using a soldering gun with a flat tip as a small hot plate upon which usually 0.02 g of sample



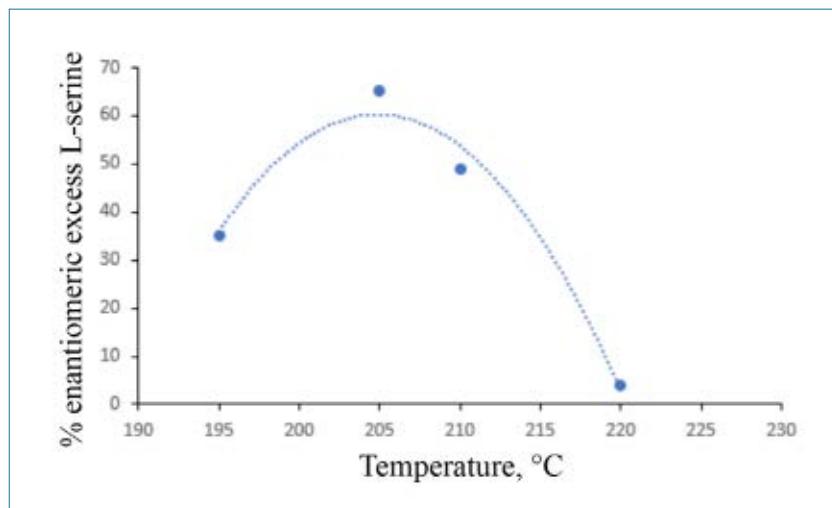
**Figure 3.** Enantiomeric excess and chemical composition of the sublimate as a function of temperature beginning with a 3% e.e.<sub>L</sub> serine sample heated for 2 h, with the heating tape held stationary. The highest chiral purity was obtained between 190 and  $205^\circ\text{C}$  (blue line). Thermolysis (red line) increased with temperature. The reported % thermolysis products were based on chromatograms of the sublimate.

was placed. The temperature was increased at a rate of  $2^\circ\text{C}/\text{s}$  from 30 to  $300^\circ\text{C}$ . The individual sublimation experiments lasted c. 90 min. The sublimation products were ionized at 5 kV and then analysed by a mass spectrometer.<sup>2</sup>

The flat tip of the soldering gun was located 1 cm below the bottom of a metal cooling funnel set up to collect products on its inner surface. A gas flow adapter was used, with dry ice ( $\sim -195^\circ\text{C}$ ), to cool the funnel.<sup>2</sup> An octamer began to form at  $\sim 180^\circ\text{C}$  and reached a maximum concentration at  $\sim 220^\circ\text{C}$ . At such temperatures, water vapour partially isolated the liquid droplet and the hot surface, decreasing the effectiveness of heat transfer.<sup>8</sup> However, the decomposition point of serine is  $\sim 222^\circ\text{C}$  according to Sigma-Aldrich, but Yablokov *et al.* found the temperature range of decomposition for serine to be  $198\text{--}222^\circ\text{C}$ .<sup>9,10</sup> Therefore, for these kinds of experiments with serine, exposure to higher temperatures has to be limited to very short time durations.<sup>2</sup>

Yang *et al.* performed experiments using isotopically labelled D- and L-serines which were sublimed.<sup>2</sup> Analysis of the products indicated that clusters of 2–8 serines formed, attached preferentially to enantiomers of the same chirality, especially for the octamers. Octamers having 8/8, 7/8, 6/8, 5/8, and 4/8 L-serines were generated.

The overall pre- and post-sublimation proportion of D- and L-serine remained unchanged, only the location of the enantiomers was modified. The authors believe the octamer



**Figure 4.** Enantiomeric excess of the sublimate at different temperatures from a 5% enantiomeric excess L-Serine sample using a moving heating tape for 18 h.<sup>3</sup>

resulted from crystal disintegration into smaller clusters, with the most stable ones surviving the high temperature. Some pyrolysis products were also incorporated successfully into octamers by replacing one or more serines.<sup>2</sup>

### Serine octamer exists in two forms

At temperatures around 150°C, solid serine sublimed mainly as monomers, but serine dimers and octamers appeared at higher temperatures.<sup>8</sup> This explains why the researchers used such a rapid rate of heating in the sublimation experiments. It was necessary to quickly pass through the lower temperature stage. Formation of chiral octamers did not occur until at least 180°C and was most significant around 220°C. But at the much lower temperatures, serines present in a prebiotic earth would have sublimed and dissipated over time. A high concentration of pure serine was required to form octamers, and these had to be trapped by an extremely low-temperature dry surface. Therefore, in these optimized experiments, the serines were rapidly exposed to temperatures around +200°C and then cooled to about -200°C within a timescale of seconds!

To emphasize the point, under the carefully controlled laboratory conditions, serine octamers exist in two isomeric forms, A and B, but only the higher temperature conformer, A, displays the desired chiral effect.<sup>2</sup> In the sublimation experiments, conformer A only begins to appear in trace amounts at ~180°C.<sup>2</sup> The homochiral and heterochiral B-type octamers which formed first were equally stable and reached a maximum concentration at ~130°C.<sup>2</sup> This temperature is much closer to the boiling point of water and to temperatures amenable to life than is ~220°C. Conformer B was also

more capable of forming octamers and larger 16-mers, 24-mers, and 32-mers metaclusters than was A.<sup>11</sup>

### Relevance to OoL speculation

Nanita *et al.* claimed that serine had been detected in experiments that simulate prebiotic conditions<sup>8,12</sup> and that serine can be formed from formaldehyde and glycine (see figure 5).<sup>13</sup>

They then concluded, “Taken together, all the experimental evidence points towards serine as a likely prebiotic molecule.”<sup>8</sup> *All the experimental evidence?* That is quite an exaggeration. In early experiments AAs were produced under allegedly relevant pre-

biotic conditions. The scientists had to assume the presence of gases leading to a reducing atmosphere. However, current geochemistry modelling denies such an atmosphere could have existed.<sup>15,16</sup>

Therefore, Miller and other chemists repeated the original Miller and Urey experiments using realistic gas mixtures, but no amino acids could be obtained.<sup>17–19</sup> Plankensteiner *et al.* subjected a mixture of carbon dioxide, nitrogen, and water to continuously supplied sparks, and the only AAs obtained were glycine and alanine, the simplest amino acids.<sup>20</sup> Worse still, the latest view is that conditions in a putative primordial earth would have led to far fewer lightning strikes than commonly assumed.<sup>21</sup>

Serine could also allegedly result from the reaction between interstellar glycine and formaldehyde (see figure 5).<sup>22,23</sup> However, serine has not been detected in outer space spectra. In the rare cases when serine was found in meteorites, it was only in trace amounts. In the extensively studied Murchison meteorite, serine was found in sub part-per-million concentration, most or all of which was considered due to terrestrial contamination.<sup>24</sup>

Assuming serine would have been available, e.e.<sub>L</sub> of serine could have been accomplished in theory by starting with an excess of L-enantiomer and running cycles of octamer formation and dissociation.<sup>8,25</sup> The n-mers formed would not have been all L, however, and no net overall e.e. would have resulted throughout nature, since only the microenvironment of the D and L serines has been modified.

In one set of experiments, the initial serine mixture contained an e.e.<sub>L</sub> of 20%, which was concentrated into octamers having an e.e.<sub>L</sub> of about 50%.<sup>8</sup> Of course there would have been no 20% excess when life was supposed to have arisen in the extremely hot aqueous conditions

following a putative Late Heavy Bombardment, between c. 4.0 and 3.8 billion years ago.<sup>26</sup> AA racemization during these millions of years would have been ensured. Suppose that somehow a 2% excess (and not the laboratory 20%) existed somewhere. The maximum excess in the octamers generated would now be irrelevant for any OoL discussion. A coincidental L-e.e. could plausibly be accompanied by a nearby D-e.e. and subsequent mixing of the products.

Experiments which used AAs such as threonine having an initial small e.e. were not reported, but, given the much lower enantioselectivities in their clusters, they would have resulted in virtually no change in e.e. in these mixed octamers.<sup>8</sup> Therefore, chiral transmission to other amino acids through substitution of serines would have a minimal and irrelevant effect, even when carried out under ideally controlled conditions.

### Incorporation of L-amino acids into serine octamers

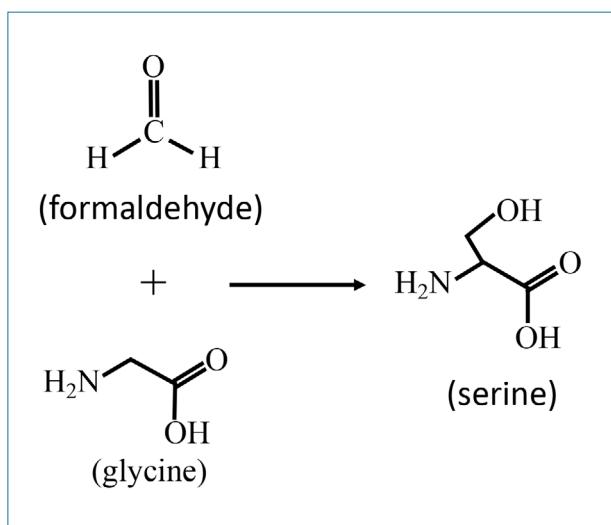
Evolutionists have claimed that octamers might have played a role in the origin of L-AAs used in primitive proteins. For example, aerosols may have formed in hot springs or waterfalls.<sup>8</sup> In a series of other experiments, Yang *et al.* examined pure L-enantiomers of each of the biological L-AAs to determine which incorporated into serine octamers.<sup>2</sup> Six L-amino acids (leucine, isoleucine, tryptophan, threonine, cysteine, and lysine) showed a preference to replace one or more L-serines in the octamer compared to the D-serines.<sup>2</sup> If D-amino acids were used with D-serine, the authors predict the mirror effect would occur. These experiments showed that octamers having mostly D or L will form. However, under alleged prebiotic ‘natural’ conditions, these octamers would be intimately mixed, leading to no spatial enantiomeric resolution.<sup>2</sup>

Since the incorporated AAs were already pure L, nothing useful has been demonstrated for OoL purposes. The results from beginning with racemic AAs or having a small e.e.<sub>L</sub> only would need to be evaluated.

### Incorporation of other organic substances in serine clusters

Experiments reported by Takats and Nanita *et al.* showed that L-serine can undergo a condensation reaction with D-glyceraldehyde, the simplest aldose, in water at ~75°C after about 14 h.<sup>14</sup> This dehydration product can substitute one or two serines in the L-octamer (about 8% abundance in the case of one Ser substitution, and 3% for two substitutions). The product of D-serine with D-glyceraldehyde was not incorporated into L-serine octamers.

There was also a chiral preference for L-serine to combine with D-glucose and of course also the opposite, D-serine



**Figure 5.** Formation of serine by reacting glycine and formaldehyde.<sup>14</sup>

with L-glucose, compared to the homoclusters.<sup>14</sup> In these examples of molecule incorporation into serine clusters, the mirror effects ensure that no net e.e. would result on average.

Although Nanita and his collaborators have seriously oversold the relevance of serine octamers for origin of life (OoL) purposes in their publications, in a key paper their final comments did state matters in more realistic terms, writing that “The presence of homochiral serine octamers in the solution and solid phases remains to be demonstrated directly, as does the existence of stable neutral octamers” and “conclusive evidence for mirror-symmetry breaking does not yet exist for any system, and serine is no exception.”<sup>8</sup>

### Critique of these studies

- Serine would be produced in only trace or no amounts under realistic, proposed prebiotic conditions. Being highly soluble in very hot water, it would readily racemize and therefore be entirely racemic and hence would display no tendency to concentrate together at some very hot location.
- If somehow highly concentrated under hot conditions, pure serines would first form octamers with a racemic content. If temperature then increased, the serines would sublime almost entirely as monomers. There is no reason why a large amount of pure serine would be enclosed in a small volume for all of it to be almost instantly exposed to a temperature ~200°C to produce octamers. Only in this highly contrived manner were the necessary high concentrations of serine generated. In a natural setting, individual serine molecules would racemize, decompose, and sublime individually over long time periods.
- There is no reason any octamers formed would not remain exposed to the high temperatures for a long period of time,

- decomposing the serines, instead of the wished-for sublimate being almost instantly cooled hundreds of degrees soon after being formed.
- Any minor e.e. generated would have been very short-lived. These would have been eventually exposed to water and dissolved back to individual serines.
  - Threonine, proline, or other amino acids replacing serines formed very weak octamers with far weaker preference to form homochiral clusters.<sup>8</sup> Non-biological sugars, AAs, and other substances could also contaminate the octamers, hindering formation of homochiral crystals.<sup>8</sup>
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# Enantiomeric amplification of L-amino acids: part 6—sublimation using Asn, Thr, Asp, Glu, Ser mixtures

Royal Truman

Much effort has been expended to explain how proteins based on only L- amino acids (AAs) could have arisen naturally. Five AAs are known to form homochiral aggregates under special conditions: Asn, Thr, Asp, Glu, and Ser. Therefore, in a key experiment critiqued here, pure L-enantiomers of each of these five AAs were mixed 97.5:2.5 with a more-volatile aliphatic AA: Ala, Leu, Pro, or Val. However, since strong L-L interactions formed in these binary mixtures, sublimation always released more of the biologically *wrong* D-enantiomer into the environment. These experiments also illustrate how unrealistic the conditions are which researchers are using for origin of life purposes. In the experiments: 1) pure L-enantiomers of only five carefully selected AAs were used, each thoroughly ground and mixed with another volatile AA; 2) sublimation was conducted at very low pressure and ideal temperature; 3) the sublimate was trapped with a cold finger before contamination with racemic AA could occur; 4) sublimation was discontinued at the ideal time to prevent subliming all the AA; and 5) experiment duration was kept short to prevent the residue from being both racemized and thermally degraded.

This is Part 6 of a series critiquing possible explanations for a natural origin of the L-amino acids (AAs) needed to form proteins. Specifically, we continue to analyze processes whereby an initial small enantiomeric excess (e.e.) of L-AAs might have been extracted and separated (amplified) through natural means into a separate location. Without enantiomerically pure L-AAs and D-sugars, cellular life cannot exist.

## Using Asn, Thr, Asp, Glu, and Ser mixtures at high temperature and low pressure

Only a few proteinogenic AAs have been shown to form homochiral aggregates, although in all cases, special laboratory conditions have been necessary.<sup>1</sup> Racemic asparagine (Asn) and threonine (Thr) crystallize from aqueous solutions as conglomerates; supersaturated solutions of mixed aspartic acid (Asp) and glutamic acid (Glu) can produce enantiopure crystals; racemic serine (Ser) can form homochiral oligomers within a narrow temperature range in the gas phase and produce an almost enantiopure aqueous solution at its eutonic point.<sup>2</sup>

Tarasevych *et al.* decided to see whether high proportions of enantiopure samples of these five AAs could separate D- and L-enantiomers of racemic mixtures of other AAs.<sup>2</sup> In the experimental setup, an aqueous solution of 975 mg enantiopure conglomerating AA was mixed with 25 mg of racemic AA, either Ala, Leu, Pro, or Val, and then the liquid was evaporated off. The solid powder was ground with a mortar and pestle and then partially sublimed during 14 hours

at 100–105°C and 0.3–0.7 mbar.<sup>3</sup> These conditions were selected to ensure that the five enantiopure AAs wouldn't also sublime.

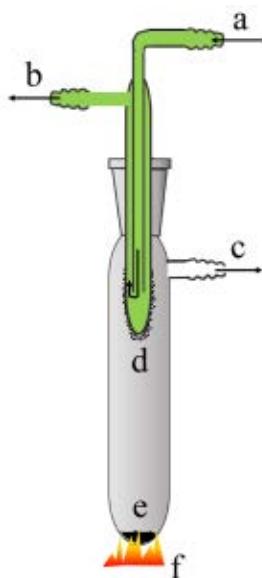
The first sublimate produced was collected from a cold finger trap (see figure 1) and analyzed by GC (gas chromatography), leading to the results shown in table 1. In all cases, using an L-enantiomer for the less-sublimed AA produced sublates with a D-enantiomeric e.e. of sublimate and vice-versa.

To confirm that L-L and D-D interactions are stronger than L-D interactions, additional experiments were carried out using enantiopure Asn mixed with different concentrations of Ala (see table 2).

Note in table 2 that pure L-Asn with D-enriched Ala led to higher e.e.<sub>D</sub> (entries 1, 2, 4, 5, and 7). Analogously, pure D-Asn with L-enriched Ala led to higher e.e.<sub>L</sub> (entries 3 and 6). Consistent with these results, pure L-Asn mixed with L-enriched Ala led to lower e.e.<sub>L</sub> values (entries 8–10).<sup>2</sup>

In the studies discussed in part 4 of this series, Viedma *et al.* proposed that the enantioenrichment of sublimate would offer a natural means to obtain higher e.e.<sub>L</sub> values for some biological AAs.<sup>4–6</sup> The experiments conducted by Tarasevych *et al.* however, produced the opposite results under other conditions, namely enantio-depletion of L-enantiomer was found in the sublimate.<sup>2</sup> This would require an entirely different Origin of Life (OoL) narrative.

The results reported by Tarasevych *et al.* implied that L-L and D-D interactions between the AAs which sublimed with those which didn't in the solid mixtures were stronger than L-D interactions. Therefore, when a large excess of pure



**Figure 1.** Cold finger apparatus used to trap sublimate. a: Inflow of coolant liquid (green); b: Outflow of coolant liquid; c: Vacuum through side-arm; d: Sublimate frozen on the cold finger; (e) Residue; f: Heat source. Artwork by R. Truman.

L-enantiomer of the heavier non-sublimating AA was used more of the lighter D-enantiomer of the AA would sublimate, and vice-versa.

OoL researchers need to show how L-enantiomers for *all* the biological AAs could have formed. However, the experiments summarized in table 1 and table 2 demonstrate that L-AAs would *lower* the L/D proportion of other AAs in the environment after they sublimated, increasing the proportion of *deleterious* D-AAs. Since this is the opposite result to that desired, what about in the residue? Given that L-L interactions are stronger, would the L/D ratio necessarily increase for the non-sublimating AA there? The researchers neglected to perform this analysis. Being at a much higher temperature than the sublimate, this material would be thermally degraded, lowering the total amount of both L-AAs present there. Furthermore, racemization would occur faster in the hotter conditions, especially upon encountering moisture, lowering the e.e. Without careful laboratory intervention to time everything just right, the process described would be a good way to eliminate excess of L-AA present in nature.

### Critique of this study

The authors wrote enthusiastically:

“The deracemisation of natural amino acids via sublimation has been accomplished for the first time.”<sup>2</sup>

This seems to be true, and they are to be congratulated. They have expertly conducted a series of well-designed

**Table 1.** Enantiomeric enrichment (e.e.) obtained by partial sublimation of binary mixtures of racemic aliphatic amino acid with an enantiopure, less-sublimating amino acid.<sup>2</sup> Temperature ~100–105°C, 14 hours, pressure 0.3–0.7 mbar. The first sublimate was collected from a cold finger by washing with 1 M hydrochloric acid. See figure 1 for the apparatus issued.

Exp	Starting mixture <sup>a</sup>	e.e. of the sublimate, % (amount, mg <sup>b</sup> )
1	L-Asn + DL-Ala	11.3–13.6 D (1–2) <sup>c</sup>
2	D-Asn + DL-Ala	10.9–15.2 L (1–2) <sup>c</sup>
3	L-Asn + DL-Val	7.6 D (3)
4	L-Asn + DL-Leu	5.5 ± 4 D (1.5) <sup>c</sup>
5	L-Asn + DL-Pro	10.7 ± 2.0 D (6) <sup>c</sup>
6	D-Asn + DL-Pro	10.8 ± 4.7. L (9) <sup>c</sup>
7	L-Ser + DL-Ala	18.5 D (4.9)
8	L-Ser + DL-Val	1.1 D (5)
9	L-Ser + DL-Leu	0.4 D (3.5)
10	L-Ser + DL-Pro	8.9 D (12)
11	L-Thr + DL-Ala	38.2 D (<1)
12	D-Thr + DL-Ala	45.7 L (<1)
13	L-Thr + DL-Val	13.9 ± 3.6 D (2) <sup>c</sup>
14	L-Thr + DL-Leu	47.1 D (<1)
15	L-Thr + DL-Pro	8.1 D (6)
16	L-Glu + DL-Ala	14.0 D (<1)
17	L-Glu + DL-Val	13.4 D (4)
18	L-Glu + DL-Leu	9.4 D (2)
19	L-Glu + DL-Pro	3.7 D (9)
20	D-Asp + DL-Ala	51.5 L (2)
21	L-Asp + DL-Val	44.0 D (5)
22	L-Asp + DL-Leu	51.2 D (~1)
23	L-Asp + DL-Pro	12.8 D (10)

<sup>a</sup> Mass of enantiopure amino acid: 975 mg; mass of the racemic amino acid: 25 mg

<sup>b</sup> Hydrochlorides

<sup>c</sup> Based on 2 or 3 experiments

experiments and discovered noteworthy results. But there is a big difference between clever chemists finding a solution to a problem and expecting this to also occur with no deliberate guidance. Here are some reasons why this work does not show that e.e. amplification would occur naturally to produce pure biologically relevant AAs.

**Table 2.** Partial sublimation of mixtures of D/L-Asn and non-racemic Ala at 100–105°C, 14 hours, pressure 0.3–0.7 mbar.<sup>2</sup> The first sublimate was collected from a cold finger by washing with hydrochloric acid.

Exp	Starting mixture <sup>a</sup>	Starting e.e. (Ala), %	e.e. of Ala sublimate, %
1	L-Asn + Ala	12 D	24.8 ± 1.0 D <sup>b</sup>
2	L-Asn + Ala	35 D	63.2 D
3	D-Asn + Ala	35 L	60.8 L
4	L-Asn + Ala	62 D	69.9 D
5	L-Asn + Ala	64 D	71.0 ± 1.9 D <sup>b</sup>
6	D-Asn + Ala	64 L	72.0 ± 3.0 L <sup>b</sup>
7	L-Asn + Ala	80 D <sup>c</sup>	89.8 D
8	L-Asn + Ala	13 L	4.3 L
9	L-Asn + Ala	25 L	12.4 ± 3.0 L <sup>b</sup>
10	L-Asn + Ala	80 L	72.9 L

<sup>a</sup> 975 mg of Asn, 25 mg of Ala

<sup>b</sup> Based on 2 or 3 experiments

<sup>c</sup> The original paper claimed 80 L, which is surely wrong. The main text confirms that 80 D was meant.

- The process can only be applied to a minority of biological AAs which sublime more easily than the five enantioenriching AAs.
- The results required the presence of 97.5% of a specific AA having 100% enantiopurity before life would have existed. This is not plausible. The AA would have been contaminated with many other substances and/or found bound in large complex molecules and not free AA.
- To avoid thermal decomposition, extremely low pressures were used, and a temperature of 100–105°C. This poses multiple problems:
  - Where on primordial earth would such conditions occur? (Atmosphere pressures are ~1,013 mbar and nowhere near 0.3–0.7 mbar!). Note that the authors claimed that their “results suggest an endogenous alternative based on the sublimation due to the presence of enantiopure materials.”<sup>2</sup>
  - Relevant for OoL models would be a time period after a putative Late Heavy Bombardment between ca. 4.0 and 3.8 billion years ago.<sup>7</sup> This event would have eliminated any e.e. in AAs. Where could this high-temperature and low-pressure environment with pure or almost pure non-volatile AAs have existed?
  - The AAs were first thoroughly mixed in aqueous solution under ambient conditions of temperature and pressure; then the water was removed. The sublimation

experiments, however, were conducted under entirely different conditions, at >100 °C and <1 mbar.

- Nature would not have provided a mortar and pestle nor anything analogous to thoroughly homogenize solids before initiating the sublimation process.
- It is not plausible that a volatile AA would have been added suddenly to a large amount of an enantiopure AA of the right kind. Under the experimental conditions, volatile AAs would have fully sublimed and dissipated long ago.
- The researchers discontinued sublimation at exactly 14 hours. Not 14 seconds or 14 millennia. Why would sublimation not have continued for a few more hours until the entire 2.5 mg had sublimed, freeing all those AAs as racemic mixtures once again?
- Under natural conditions nothing would have prevented the sublimate and residue from simply remixing.

Clearly this research offers no support that excess L-AAs could have arisen naturally. An important lesson from studies like these is that under very unnatural conditions it is sometimes possible to separate L-AAs and at other times D-AAs temporarily. The effects are negligibly small and, without deliberate experimental guidance, tend to cancel, hindering formation of a net e.e.<sub>L</sub>.

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# Developments in paleoanthropology no. 4

Peter Line

This paper discusses some recent developments in paleoanthropology from a creationist perspective. This includes newly reported evidence indicating *Homo naledi* buried their dead, made engravings, and used tools. Given *H. naledi*'s small brain size, the relationship between brain size and intelligence is examined, as is the cranial capacity of some specimens. Cretinism as an explanation for *H. naledi* is discussed. Also looked at is a report that modern humans were in Laos earlier than thought. Oldowan-like tools produced unintentionally by monkeys are investigated. Recent news on Neanderthals is also presented.

## Evidence *Homo naledi* buried their dead, made engravings, and used tools

The previous paper in this series discussed newly found evidence, presented by paleoanthropologist Lee Berger, indicating *Homo naledi* used fire in the Rising Star cave system, South Africa.<sup>1</sup> On 5 June 2023, at the Richard Leakey Memorial Conference at Stony Brook University, Berger announced that he and his team had also discovered evidence suggesting *H. naledi* buried their dead, made symbolic engravings on cave walls, and used stone tools. The findings were also detailed in three papers made available on the preprint server *bioRxiv* on the same day.<sup>2-4</sup> These papers, after review, will be published in the online journal *eLife*. In the paper dealing with evidence for deliberate burial, Berger *et al.* stated:

“Recent excavations in the Rising Star Cave System of South Africa have revealed burials of the extinct hominin species *Homo naledi*. A combination of geological and anatomical evidence shows that hominins dug holes that disrupted the subsurface stratigraphy and interred the remains of *H. naledi* individuals, resulting in at least two discrete features within the Dinaledi Chamber and the Hill Antechamber. These are the most ancient interments yet recorded in the hominin record, earlier than evidence of *Homo sapiens* interments by at least 100,000 years.”<sup>5</sup>

In the Hill Antechamber, Berger *et al.* said that the “combination of these lines of evidence indicates that a pit was dug into existing strata, and then a body was placed into it and buried prior to the decomposition of soft tissue.”<sup>6</sup> Similar lines evidence were found for the burial in the Dinaledi Chamber, with the skeletal elements exposed within the burial feature said to be “anatomically consistent with *H. naledi*”.<sup>7</sup> The configuration of the skeletal remains in the Hill Antechamber was said to be consistent with the body (of Individual 1) being in a flexed position when interred.<sup>8</sup> The authors stated:

“The existence of diverse practices in the placement or interment of individuals within the Rising Star cave system is similar to the diverse practices noted within

other sites of multiple burials of *H. sapiens* including Qafzeh Cave and Skhūl Cave.”<sup>9</sup>

According to Berger *et al.*, the evidence suggested that “diverse mortuary practices may have been conducted by *H. naledi* within the cave system”, and that “mortuary practices were not limited to *H. sapiens* or other hominins with large brain sizes.”<sup>10</sup> They pointed out that some “authors have argued that mortuary behavior is unlikely for *H. naledi*, due to its small brain size”, but that the “evidence demonstrates that this complex cultural behavior was not a simple function of brain size.”<sup>11</sup>

A single stone artifact was discovered in the Hill Antechamber burial feature, said to be “in close contact with the articulated hand and wrist material”.<sup>12</sup> This artifact (figure 1), called the Hill Antechamber Artifact 1 (HAA1), is described as having striations visible on the surface “that appear to be use wear or erosional marks”.<sup>13</sup> In the accompanying Berger *et al.* paper on rock engravings, the artifact is described as a tool-shaped rock that resembles “tools from other contexts of more recent age in southern Africa, such as a silcrete tool with abstract ochre designs on it that was recovered from Blombos Cave”.<sup>14</sup>

The engravings (figure 2), said to be on a natural pillar (dolomitic walls) forming “the entrance and exit of a passage connecting the Hill Antechamber with the Dinaledi Chamber”, are described as mostly linear makings, with many of them intersecting “to form geometric patterns such as squares, triangles, crosses, and X’s, while some are isolated lines.”<sup>15</sup> According to the authors there is no evidence of modern cavers altering the cave walls in such a manner in the Rising Star system, and that

“It is unlikely that any other hominin population made these engravings. No physical or cultural evidence of any other hominin population occurs within this part of the cave system, and there is no evidence that recent humans or earlier hominins ever entered any adjacent area of the cave until surveys by human cave explorers during the last 40 years.”<sup>16</sup>



**Figure 1.** The Hill Antechamber Artifact 1 (HAA1) is described as a tool-shaped rock. Shown are “striations visible on both faces and intersection of these striations with sharp edge of artifact showing appearance of serrations.”

Berger *et al.* believe that *H. naledi* is “the most likely creator of these engravings”, and that this “has implications for the evolution of biological intelligence among hominins and the association with [sic] encephalization with cognitive complexity.”<sup>17</sup> In the third *bioRxiv* paper, dealing with the evolutionary implications of the above findings, Fuentes *et al.* stated:

“Fire use, mortuary behavior, and the evidence of engravings attributed to *H. naledi* falsify the hypothesis that only a large-brained hominin was capable of cognitively complex cultural, possibly symbolic, behavior.”<sup>18</sup>

The reaction by evolutionists to these latest announced findings about *H. naledi* has been mixed. Writing in *New Scientist*, Alison George quotes one researcher (Emma Pomeroy) as saying, “It is premature to conclude that symbolic markings were made by small-brained hominins, specifically *H. naledi*”.<sup>19</sup> Another expert (Paul Pettitt) was unconvinced that a deliberate burial had been demonstrated by the Berger team, while Chris Stringer found the evidence impressive.<sup>19</sup> Petraglia *et al.* question the evidence supporting burial, the association of the rock art with *H. naledi*, and suggest that the stone artifact “may actually be a natural rock and not culturally modified.”<sup>20</sup>

However, one suspects that the main objection to the burial evidence is that, in the words of Petraglia *et al.*, it “implies intentional burial wasn’t limited to our species or other big-brained hominins”, and so “would force us to rethink the role of brain size in advanced ‘meaning-making’ cognition”.<sup>20</sup> That they doubt the rock art was made by *H. naledi* seems also to be influenced by the implications it has, as indicated in their statement, as follows:

“This claim has major implications. To date, rock art has only reliably been linked to *Homo sapiens* and, in rarer cases, some of our large-brained ancestors. Similar to deliberate burial, producing rock art has major implications for the cognitive abilities of a species. It denotes a capacity for representation, and the creation and communication of meaning via abstract symbols.”<sup>20</sup>

Clive Finlayson, of the Gibraltar National Museum, is quoted by Ann Gibbons as saying, “It’s not about brain size but how the brain is structured”.<sup>21</sup> He is said to believe the rock art etchings were most likely the work of *H. naledi* as no remains of “big-brained humans have been found in the cave.”<sup>21</sup>

### Brain size and intelligence

The findings announced by the Berger team are both sensational and controversial. As indicated above, one of the main objections that some evolutionists have in accepting the findings that, in the Rising Star cave system, *H. naledi* used fire, made rock art, and buried their dead, appears to be its small brain size. This is because it conflicts with their current theories on the relationship between brain size and intelligence in supposed hominins.

Evolutionary theory concludes that *Homo erectus* people (in this case *H. naledi*) had smaller brains because they were not as evolved as modern humans, making them ‘ape-men’ of less intelligence. Evolutionists suggest it may have been selection pressures for some form of intelligent behaviour that drove the brain expansion in supposed hominins like *H. erectus*. This ‘intelligence’ could have been making more sophisticated tools for hunting, being better at forming alliances through social interaction, being more efficient at communicating with language, being better at thinking with symbols, etc. According to paleoanthropologist Ian Tattersall:

“Brain tissue is metabolically expensive, so there must have been some very considerable advantage to larger brains. Presumably the dividend was received in terms of greater ‘intelligence,’ although precisely what this might have meant in terms of abilities or context remains unclear.”<sup>22</sup>

Apart from making the unproven assumption that evolution has occurred, such theories also presume that more brain tissue equals more intelligence. This seems to run counter to what is written in a popular anatomy and physiology textbook:

"Brain size varies considerably among individuals. The brains of males are, on average, about 10 percent larger than those of females, due to differences in average body size. No correlation exists between brain size and intelligence. Individuals with the smallest brains (750 mL) and the largest brains (2,100 mL) are functionally normal."<sup>23</sup>

As an example, consider the following statement by Harry Shapiro:

"Although Anatole France is said to have had a cranial capacity of only a little over 1,100 c.c. and Von Hindenburg, more than 1,800 c.c., it would certainly not be the general judgment that Anatole France was the less intelligent."<sup>24</sup>

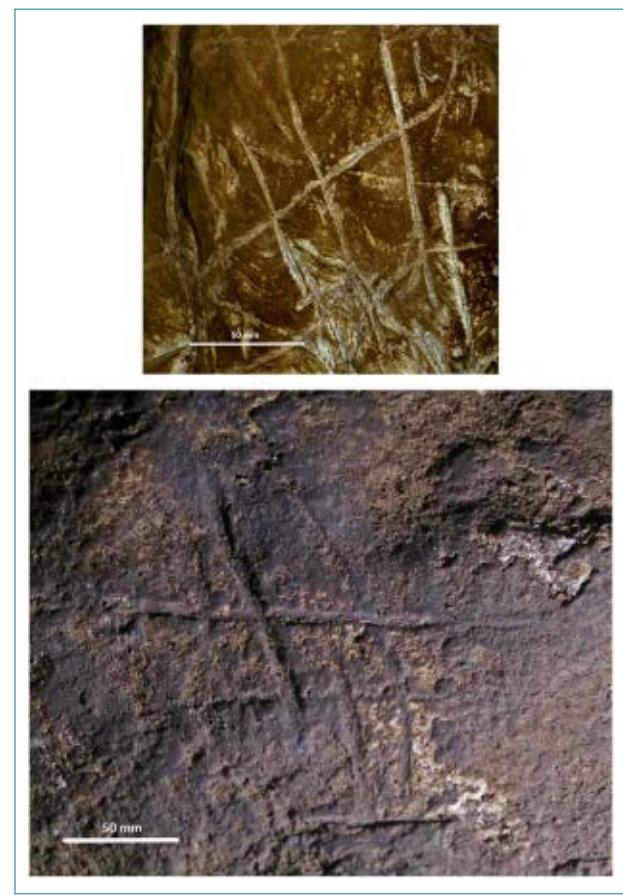
To illustrate the last point, Anatole France won the 1921 Nobel Prize for Literature, and so having a brain size within the *H. erectus* range did not appear to disadvantage him. In his biological anthropology textbook, John Relethford suggested that "there might have been a strong relationship between relative brain size and intelligence in early human evolution that is no longer in effect."<sup>25</sup> What happened to the evolutionist's motto 'the present is the key to the past'? Claims that, despite there being no relationship between brain size and intelligence now, somehow there was in the past, sounds like special pleading.

To put all this in perspective, a huge variation in brain size exists in modern humans without any noticeable correlation between brain size and intelligence. However, we are to believe that within the genus *Homo*, during the period of alleged human evolution, there was supposedly selective value for intelligence in what amounts to an increase, on average, of a few pinheads of brain tissue per generation.<sup>26</sup> Rather, if there is no significant link between brain size and intelligence, then brain size increase would have no selective value in any alleged environment of evolutionary adaptedness. Without any significant selective value, large brain size could not have been a result of evolution even if evolution were possible (which it is not), particularly considering the high metabolic energy costs of big brains.

The small brain size is likely also the main reason some non-evolutionists object to accepting *H. naledi* as being human. They would likewise reject the evidence presented by Berger, as no non-human would create art, bury their dead, or use fire. Brain size, as indicated by cranial capacity, is examined further below.

### Cranial capacity

The mean cranial capacity of *H. naledi* is 545 cc, obtained from three specimens (DH 1—560 cc; DH 3—465 cc; LES 1—610 cc), with a range of 465 to 610 cc.<sup>27</sup> The mean cranial capacity of the Dmanisi, Georgia, *H. erectus* specimens (D 2280—730 cc; D 2282—650 cc; D 2700—601 cc; D 3444—641 cc; D 4500—546 cc) is 633.6 cc, with a range

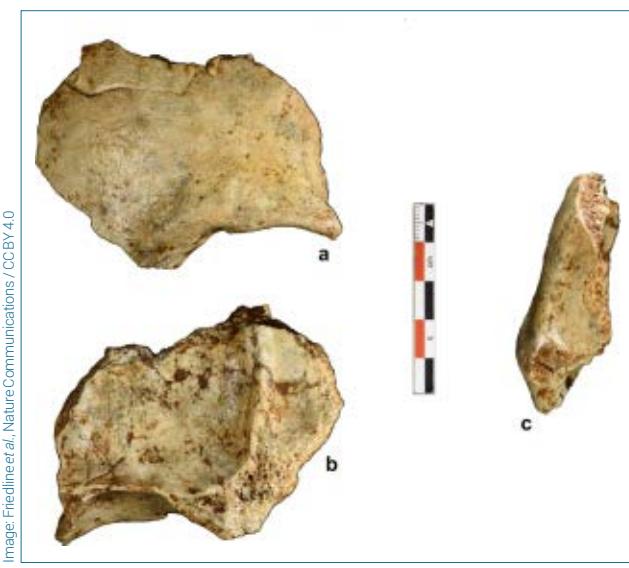


**Figure 2.** Engraving (etched crosshatch) attributed to *Homo naledi* in the Rising Star Cave system (top) compared to crosshatch engravings from Gorham's Cave, Gibraltar (bottom) attributed to a Neanderthal.

of 546 to 730 cc.<sup>28</sup> The adult *H. erectus* DAN5/P1 cranium from Gona, Afar, Ethiopia, with a cranial capacity of 598 cc, is the smallest of any adult *H. erectus* specimen from Africa.<sup>29</sup> The DAN5/P1 cranium was found in direct association with both Oldowan and Acheulian stone tools.<sup>30</sup>

Another small *H. erectus* cranium (DNH 134) was reported on in 2020.<sup>31</sup> The juvenile DNH 134 was discovered in the Drimolen Main Quarry in South Africa and dated at between an alleged 1.95 to 2.04 Ma (million years ago).<sup>32</sup> According to Herries *et al.* "DNH 134 represents the oldest fossil with affinities to *H. erectus* in the world".<sup>33</sup> The cranial capacity of DNH 134 was estimated at 538 cc, and, assuming an age at death between 2 and 3 years, the authors estimated that the DNH 134 individual could have reached an adult cranial capacity between 588 and 661 cc according to a human model.<sup>34</sup>

There are convincing arguments that the adult SK 847 cranium from Swartkrans, South Africa, is *H. erectus*, rather than the *Homo habilis* category it is often classified in.<sup>35</sup> On the status of SK 847, paleoanthropologist Ronald Clarke stated, in 1985, that "the *erectus*-like morphology of the



**Figure 3.** Photograph of the modern human TPL 6 frontal bone from Tam Pà Ling, Northern Laos. It is said to be the oldest cranial fossil recovered from the site: (a) anterior view; (b) endocranial surface; (c) left lateral view.

frontal bone (which is not seen in any of the *H. habilis* crania) plus the remarkable overall similarity to 3733 [classified as *H. erectus*] convinces me that 847 must now be classified as an early *H. erectus*.<sup>36</sup> On the brain size of SK 847, due to the incompleteness of the specimen, which has most of its neurocranium missing, any estimate of its cranial capacity would be very inaccurate, although it is likely to be very small.<sup>37</sup>

The allocation of DNH 134 to *H. erectus* raises the question of whether the specimens allocated to *H. naledi* should also be subsumed into this category. This is especially so given that the Rising Star cave system, where the *H. naledi* fossils were found, is only about 800 m from Swartkrans,<sup>38</sup> where the *erectus*-like SK 847 specimen was discovered, and 7–8 km from the Drimolen site,<sup>39</sup> where DNH 134 was found. The closeness of the three sites to each other, and their commonality of small brain size, suggest there is a connection between the specimens (ignoring their evolutionary assigned ages).

As for cranial capacity, Tobias reported a mean of 1,345 cc for modern humans ( $n = 1,000$ s; range: 800—2,100 cc).<sup>40</sup> However, it stated that this was for males (whether this was a print error I do not know). Beals *et al.* reported that the cranial capacity of 122 recent ethnic groups yielded means of 1,272 cc and 1,427 cc for females and males, respectively, with a sex-combined mean of 1,349 cc (range: 1,070–1,651 cc).<sup>41</sup> Molnar gives the mean cranial capacity for ‘modern man’ as 1,345 cc, with a range of approximately 700–2,200 cc.<sup>42</sup> According to Molnar, “These individuals with larger or smaller cranial capacities are normally functioning

and intellectually competent individuals; in fact, there are many persons with 700 to 800 cubic centimeters.”<sup>43</sup>

The smallest cranial capacity that I am aware of, from a modern human (Daniel Lyon, a man of 1.55 m height and 65.8 kg weight) with ‘normal’ intelligence, was about 660 cc or 694 cc, depending on the method used to estimate it.<sup>43</sup> The mean of 677 cc is perhaps the best estimate. However, only a minuscule number of cranial capacities of individuals have been measured/estimated compared to the billions of ‘modern’ humans that have lived, or currently live. Hence, it is difficult to know what exactly the lower limit of cranial capacity for ‘normal’ intelligence is. Statistically speaking, it seems reasonable to suggest that there would be modern humans with ‘normal’ intelligence that have (or had) cranial capacities in the *H. naledi* range.

Crania classified as *H. erectus* have on average smaller cranial capacities compared to modern humans, although there is a certain amount of circular reasoning in this, as crania tend to be excluded from the *H. erectus* category if their brain size is considered too large.<sup>44</sup> Including only crania evolutionists would typically assign to *H. erectus*, I calculated the mean cranial capacity of 50 *H. erectus* crania to be about 926 cc (range: 546–1,260 cc).<sup>45</sup> In theory, *H. naledi* could just be a population of *H. erectus*-type humans with small brains. However, the situation may not have been that simple, as discussed below.

### Cretinism and *Homo naledi*

I have discussed the *H. naledi* finds in much more detail elsewhere.<sup>46,47</sup> To recap in a nutshell, my interpretation of *H. naledi* is that it likely consisted of *H. erectus*-type ‘robust’ humans (descendants of Adam and Eve), some of whom suffered from a developmental pathology called ‘cretinism’. This could possibly explain some of the odd morphological features present in some of the fossil specimens, including the small brain size. From a creationist viewpoint, all specimens genuinely belonging to *H. erectus* should ultimately be reclassified as *H. sapiens* if *H. erectus* individuals were fully human, i.e. descendants of Adam and Eve.

Some evolutionist experts have postulated that the bones of the Indonesian *Homo floresiensis* represent cretinism in humans.<sup>48</sup> The cranial capacity of 426 cc, for the LB 1 *H. floresiensis* specimen,<sup>49</sup> is smaller than any of the published values for *H. naledi*. Cretinism has major developmental effects, causing bony deformities, mental retardation, and more, and is caused by iodine deficiency in the unborn. It is common in areas with low environmental iodine, where there is also a high incidence of adult goitre (thyroid enlargement, thus neck swelling, from insufficient iodine).<sup>50</sup> The ‘Cradle of Humankind’ area, where the *naledi* fossils were found, is located on or near the fringes of what was, prior to iodine supplementation, a narrow ‘goitre belt’, or region in which this deficiency disease was

very common. The belt ran 500 km across South Africa's Transvaal from Zeerust to Nelspruit.<sup>51</sup> This regional history increases the likelihood of cretinism in these fossils. Only a small percentage of the population in a 'goitre' region were usually affected by cretinism.

Cretinism (congenital hypothyroidism) "can reduce brain size by approximately 50%",<sup>52</sup> and so would be one possible explanation for the low cranial capacity observed in the *H. naledi* crania, as well as some of the other small *H. erectus* crania. To me, the evidence for burials in the Rising Star cave system appears convincing. As humans only go to the trouble of burying other humans (not apes), this indicates that the buried *H. naledi* remains were those of humans.

What is not clear is whether the *H. naledi* remains, in the Rising Star cave system, represent both pathological and non-pathological members of the population, if indeed some had suffered from cretinism. It could be that only pathological humans were buried in the remote cave system. Perhaps that was the very reason they were given a burial in such a remote place. Regardless, it is likely that any burial practice was done by healthier members of the population, the latter perhaps also having larger brain sizes, although this can only be speculation. However, if the evidence indicating *H. naledi* buried their dead, used fire, made symbolic engravings, and used stone tools, is confirmed, then *H. naledi* individuals were fully human, whether they had small or large brains.

### Modern humans in Laos earlier than thought

On 5 June 2023, a study on recently discovered *Homo sapiens* bone fragments was published, titled "Early presence of *H. sapiens* in Southeast Asia by 86–68 kyr at Tam Pà Ling, Northern Laos".<sup>53</sup> That modern humans may have been in Southeast Asia between 68 and 86 thousand years ago (ka) is said to be "considerably further back than the previous estimates of around 50,000 years".<sup>54</sup> The modern human bone fragments in question were recently discovered frontal (TPL 6; figure 3) and tibial (TPL 7) fragments found in the deepest layers of the Tam Pà Ling (TPL) cave site.<sup>53</sup> Previous discoveries in the cave were said, by Freidline *et al.*, to have identified *H. sapiens* there by supposedly at least 46 ka.<sup>53</sup> According to Jude Coleman:

"The shape of the Tam Pà Ling fossils further complicates the story. Although they are from *H. sapiens*, the youngest bone—the 46,000-year-old skull fragment—has a mixture of characteristics of both archaic and modern humans, whereas the oldest fossils have more-modern features. For example, the older skull fragment lacks the pronounced brow bone associated with more-archaic humans that is observed to some degree in the younger fossil."<sup>55</sup>

Coleman further writes, "That is counter-intuitive, Shackelford [co-author of study] says, and suggests the older fossils might not have evolved from local populations,

but rather represent groups of early modern humans that migrated through the area."<sup>55</sup> What it does suggest is that the so-called 'archaic' humans and 'modern' humans were interbreeding with each other. This appears to have been a common occurrence. In their overview of the fossil evidence, Cartmill and Smith stated that "in southern and northern Africa, East Asia, Australasia, and Europe, early modern populations retained a few morphological characteristics that evidently derived from local archaic peoples."<sup>56</sup> This indicates that 'modern' humans and 'robust' ('archaic') humans interbred, and so had to be of the same biological species. Not only do evolutionary explanations add nothing, rather they obscure the truth of human history. As for the dating, Freidline *et al.* throw doubt on fossils predating 50 ka from Chinese sites, stating:

"A recent attempt to verify the dating of several of these sites by Sun *et al.* ... presented a number of issues including inaccurate radiocarbon estimations, misattribution to *Homo* of a sampled tooth, potential contamination in genetic analyses and incorrect provenience".<sup>57</sup>

To be sure, the Sun *et al.* paper does not inspire confidence in the dating of Chinese sites when it reports the following:

"Some paleoanthropologists have argued that fossil discoveries from Huanglong, Zhiren, Luna, and Fuyan caves in southern China indicate one or more prior dispersals, perhaps as early as ca. 120 ka. We investigated the age of the human remains from three of these localities and two additional early AMH sites (Yangjiapo and Sanyou caves, Hubei) by combining ancient DNA (aDNA) analysis with a multimethod geological dating strategy. Although U–Th dating of capping flowstones suggested they lie within the range ca. 168 to 70 ka, analyses of aDNA and direct AMS <sup>14</sup>C dating on human teeth from Fuyan and Yangjiapo caves showed they derive from the Holocene. OSL dating of sediments and AMS <sup>14</sup>C analysis of mammal teeth and charcoal also demonstrated major discrepancies from the flowstone ages; the difference between them being an order of magnitude or more at most of these localities."<sup>58</sup>

Freidline *et al.* appear to have had their own dating issues, with optically stimulated luminescence (OSL) samples producing a similar age when taken from different sediment depths.<sup>59</sup> Suggesting that "the age of the deepest layers are underestimated due to the saturation limits of quartz OSL dating that occurs at 3–4m", they then used another dating technique (pIR- IRSL<sup>60</sup>) in the deeper layers as "an independent age control".<sup>59</sup> Using more than one dating technique also makes it easier to cherry-pick data. I have no confidence in the ages obtained using any of these dating techniques as, apart from all the discrepancies, they also make invalid assumptions. Coverage of the problems, flawed assumptions,

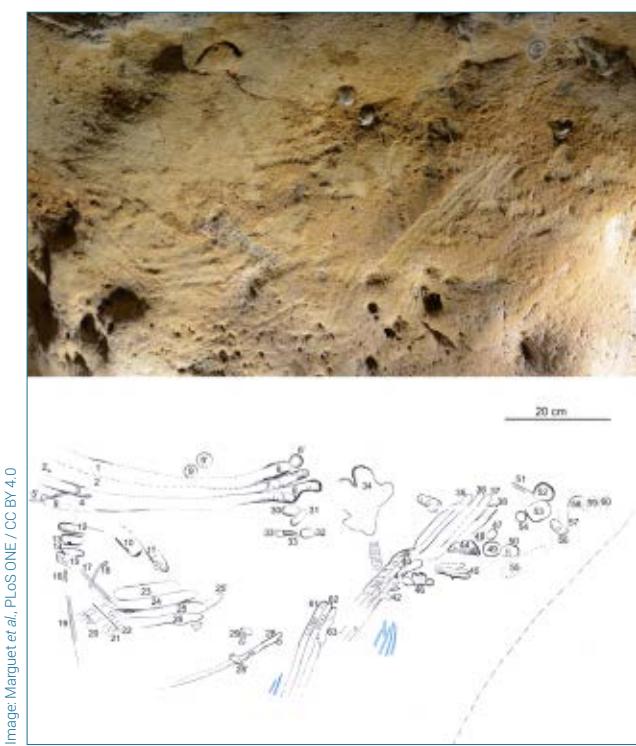


Image: Marguet et al., PLoS ONE / CC BY 4.0

**Figure 4.** The Linear Panel. Neanderthal engravings on a cave wall at La Roche-Cotard, France. “The limits of the finger flutings are shown in black. When the edges are well cut, the line is thicker. When the line is not clearly legible, the line is dashed. Animal tracks are in blue. ... The survey (J. Esquerre and H. Lombard) gives the numbering of the traces.”

unknowns, and unreliability of age-dating methods is available elsewhere.<sup>61,62</sup> I suspect the most interesting dates are the ones we do not see because they are not published.

### Stone artefacts by monkeys

A study by Proffitt *et al.*, published 10 March 2023, reported on the lithic assemblage associated with foraging behaviour of wild long-tailed macaque monkeys in Thailand, said to result “in a landscape-wide record of flaked stone material, almost indistinguishable from early hominin flaked pieces and flakes.”<sup>63</sup> According to the authors:

“It is now clear that the production of unintentional conchoidal sharp-edged flakes can result from tool-assisted foraging in nonhominin primates. Comparisons with Plio-Pleistocene lithic assemblages, dating from 3.3 to 1.56 million years ago, show that flakes produced by macaques fall within the technological range of artifacts made by early hominins. In the absence of behavioral observations, the assemblage produced by monkeys would likely be identified as anthropogenic in origin and interpreted as evidence of intentional tool production.”<sup>63</sup>

Commenting on the find in *Science*, Morell wrote:

“Nevertheless, the study serves as a caution to archaeologists, says Rick Potts, a paleoanthropologist and stone tool expert at the Smithsonian Institution. ‘As tiny and unintentional as these flakes may be, they are similar to those from early archaeological sites. That means we have to find a way to factor [them] out at Oldowan sites.’”<sup>64</sup>

Discussing the find in *Scientific American*, Zorich stated:

“Their analysis revealed a surprising fact: The flakes that the macaques unintentionally produced looked a lot like the oldest stone tools that were intentionally made by hominins: Lomekwan and Oldowan stone tool assemblages, which were discovered at sites dating between 3.3 million and 1.5 million years ago. ‘If we would take the kind of assemblage that we find with the macaques and we would drop them somewhere in East Africa, everybody would think they were definitely made by early hominins,’ Luncz [co-author of study] says.”<sup>65</sup>

Previously (in 2016), the research group had reported on wild bearded capuchin monkeys in Brazil, said to have been observed deliberately breaking stones, “unintentionally producing recurrent, conchoidally fractured, sharp-edged flakes and cores that have the characteristics and morphology of intentionally produced hominin tools.”<sup>66</sup> As reported by Callaway in *Nature*, to Proffitt’s (first author) eye, many of the stone pieces broken off by the capuchins “resembled the kind of sharp ‘flakes’ first recovered by Leakey in Olduvai Gorge, Tanzania, in the 1930s”, supposedly dating from about 2.5 to 1.7 Ma.<sup>67</sup> Callaway further stated:

“About half of the flakes made by the capuchins bore the hallmarks of Oldowan tools called choppers, says Proffitt. One set of flakes seemed to have been broken off of the same hammer stone in succession, ‘something that’s only ever been associated with humans’, says Proffit [sic]. Yet he emphasizes that the monkeys make the tools unintentionally and ‘at no point do they use these flakes. They’re just hitting stones together’.”<sup>67</sup>

If Oldowan-like tools can be produced unintentionally this easily, it makes one wonder whether some (not all) of the so-called Oldowan tools were simply accidental by-products of stone breakage, and not necessarily by human hands. While the above unintentional ‘tools’ were produced by monkeys, it is possible that extinct apish primates, like the australopithecines (which includes most specimens attributed to *H. habilis*), had similar rock-breaking practices, resulting in unintentional ‘tools’. This suggests caution against reading too much into simple Oldowan-type tools found in geological strata associated with australopithecine fossils. The tools may have been unintentional by-products of breaking stones, whether by them or some other primate (e.g. monkeys). Neither can it be ruled out that catastrophic flows during Flood runoff also produced such Oldowan-type ‘tools’ in gravel. If the tools really look like they could not have been

unintentionally produced, then this would indicate they were made by humans.

### Neanderthal news

The creationist belief that Neanderthals were fully human, descendants of Adam and Eve, has already been vindicated.<sup>68</sup> For that reason it seems less necessary to cover Neanderthal news. However, they should not be ignored either, so here are, in brief, some recent items of interest on Neanderthals.

The 6 January 2023 front-page headline of *Newsweek* was titled “How We Became Human”, and, in the feature article, author Adam Piore stated:

“These and other finds, together with advanced technology that’s become available to paleontologists within the last decade, have smashed the popular conception of Neanderthals as hairy, primitive, knuckle-dragging cavemen who carried clubs and spoke in grunts. Neanderthals, we now know, were likely more intelligent, sophisticated and complicated than previously believed.”<sup>69</sup>

Piore quoted ancient DNA expert Svante Pääbo as saying that “I would tend to think that Neanderthals individually may have been as smart as us,” but that he believed modern humans were better at former bigger societies, leading to things like more innovations, although he admitted this was only speculation.<sup>70</sup> Piore also stated that Pääbo found it “hard to imagine that between 70,000 or 100,000 years ago, a new mutation spread that suddenly made everybody ‘smarter.’”<sup>71</sup> Such ‘smart’ mutations are popular in some evolutionary circles. For example, in Yuval Noah Harari’s book *Sapiens: A brief history of humankind* it was called the “Tree of Knowledge mutation”.<sup>72</sup> I critiqued such ‘magic bullet’ mutations in my review of Harari’s book.<sup>73</sup>

A study (published 1 February 2023) of the skeletal remains of straight-tusked elephants, the largest terrestrial mammals of the alleged Pleistocene epoch, excavated from deposits supposedly 125 ka, were said to show “that hunting of elephants weighing up to 13 metric tons was part of the cultural repertoire of Last Interglacial Neanderthals there”.<sup>74</sup> In *Science*, Andrew Curry commented on the find, as follows:

“The degree of organization required to carry out the butchery—and the sheer quantity of food it provided—suggests Neanderthals could form much larger social groups than previously thought.”<sup>75</sup>

Regarding the above finding, Curry quoted archaeologist Gary Haynes as saying, “This lets us imagine Neanderthals as more like modern humans rather than as humanoid brutes, as they once were interpreted.”<sup>75</sup>

On 21 June 2023 Marquet *et al.* published a study of Neanderthal engravings (figure 4) on a cave wall at La Roche-Cotard, France, made supposedly at least 57 ka.<sup>76</sup> According to the authors, typical Mousterian lithics were found in the cave, these said to be uniquely attributed to

*Homo neanderthalensis* in Western Europe.<sup>77</sup> They concluded that the cave engravings were “unambiguous examples of Neanderthal abstract design.”<sup>77</sup> Writing in *New Scientist*, Marshall commented on the engravings (made on tuff, a soft rock), said to be “some of the oldest known examples of Neanderthal art and are possibly the very oldest”:

“These include a great many lines traced by fingers: often straight lines, but sometimes also circles or ovals. Some seem to be arranged in larger patterns. One panel has a cluster of more than 100 dots. A subgroup of the engravings was made with tools like flint, antler and wood rather than with fingertips.”<sup>78</sup>

Marquet *et al.* describe the finger tracings at La Roche-Cotard as clearly intentional, but that “it is not possible for us to establish if they represent symbolic thinking”.<sup>79</sup> The authors concluded their discussion of the study with the following sentence:

“In terms of culture, we now have a better understanding of the plurality of Neanderthal activities, attesting to elaborate and organized social behaviours that show no obvious differences from those of their contemporaries, Anatomically Modern Humans, south of the Mediterranean.”<sup>80</sup>

A study by Schmidt *et al.*, published 22 May 2023, addressed how birch tar (a glue) was made by Neanderthals. They said it was the “oldest synthetic substance made by early humans”, with the earliest such artefacts associated with Neanderthals.<sup>81</sup> As described by Jackson, birch tar “was used as an adhesive backing to connect stone to bone and wood in tools and weapons, with the added benefit of being water-resistant and resistant to organic decomposition.”<sup>82</sup> From their study, Schmidt *et al.* stated:

“... we found that Neanderthals did not use the simplest method to make tar. Rather, they distilled tar in an intentionally created underground environment that restricted oxygen flow and remained invisible during the process. This degree of complexity is unlikely to have been invented spontaneously. Our results suggest that Neanderthals invented or developed this process based on previous simpler methods and constitute one of the clearest indicators of cumulative cultural evolution in the European Middle Palaeolithic.”<sup>81</sup>

At the end of his article reporting on the above study, Jackson wrote:

“The evidence for cognitively complex Neanderthals has only increased in recent years, as archaeological evidence reveals many of the technological firsts thought to be modern human inventions were already in use among Neanderthals. At this point, it may benefit anyone who prefers thinking of human intelligence as an exceptional uniqueness to concede that Neanderthals were humans too.”<sup>82</sup>

### Homo naledi update

On 12 July 2023, just after I had finished a draft of this article, the peer review and assessment by *eLife*, as well as response by the Berger team, were published on the *eLife* site.<sup>83–85</sup> The peer review was generally negative. A few technical issues were brought up, particularly regarding the burials, which the authors addressed in their response, but there was nothing refuting the main findings. I got the impression that it was the implications of the findings that were the bigger problem. For example, on the rock engraving paper, Reviewer 1 commented:

“This is a big claim. If it proves to be true, it has the potential to be paradigm-shifting as the identification of intentional engraved marks, made by a small-brained distant human cousin 200,000+ years ago in South Africa, would completely change our understanding of where, when and who made the first graphic marks. Twenty years ago, this claim would probably have been dismissed out of hand as being too far-fetched to be taken seriously”<sup>84</sup>

Hence, the two main issues appear to be the small brain of *H. naledi* and the unknown date of the rock engravings. I addressed the small brain earlier in this article. The alleged geological age of the *H. naledi* fossils and, by association, the age of the engravings, is something I do not accept. The reviewers had problems with the latter. For example, on the Fuentes *et al.* contexts and evolutionary implications paper, Reviewer 1 commented:

“The author of the engravings needs to be demonstrated as a particular hominin species (*H. naledi* in this case), and the activity of engraving needs to have taken place ~241–335 kya. After reading the manuscript on the engravings, however, what is clear is that the scratches could as easily have been made by a modern-day farmer 50 years ago, as *H. naledi*~335 kya. Berger and colleagues do not present any evidence to the contrary, they simply describe their narrative as the most parsimonious scenario.”<sup>85</sup>

I see the most parsimonious scenario as being that *H. naledi* individuals made the engravings on the rock walls in the Rising Star cave system. However, I believe it occurred much more recently than suggested by the Berger team.

### Conclusions

Evidence suggesting *H. naledi* buried their dead, made symbolic engravings on cave walls, and used stone tools was greeted with mixed reaction by evolutionists. A main objection appears to be the small brain size of *H. naledi*. *H. naledi* likely consisted of *H. erectus*-type humans (descendants of Adam and Eve), some of whom suffered from a developmental pathology called ‘cretinism’.

A study reporting that modern humans were in Laos earlier than thought suggests that so-called ‘archaic’ humans and ‘modern’ humans were interbreeding.

If Oldowan-like tools could be produced unintentionally by monkeys, perhaps some of the so-called Oldowan tools were simply accidental by-products of stone breakage.

As more studies on Neanderthals are done, the more sophisticated they appear to have been.

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# The origin of large arcs: part 2—impacts can form large arcs

*Michael J. Oard*

Large arcs are common, yet mysterious, features. A variety of proposed mechanisms leave no definitive explanation. Impacts usually create a deep basin encircled by a large circular or arcuate rim, often formed by thrusts that verge outward from the centre. All the solid bodies in the solar system that have not been resurfaced with lava or debris display this unique signature. Secular scientists have documented about 200 impacts on the earth, but there is evidence of more when proposed impacts, basins, and impact spherules in sedimentary rocks are added. The Chicxulub impact typifies problems with identification, with evidence obscured by subsequent tectonics, volcanism, erosion, and deposition. Use of the moon as an analogy results in overestimating the number of impacts on Earth. A better estimate is found in the high ratio of ‘proposed’ impacts to known impacts. A conservative estimate is 500 continental Earth impacts. Since large impacts would devastate Earth, they likely happened during the Flood, except for a few small impacts afterwards. It is even possible that impacts could have caused the Flood. If so, they could help define the pre-Flood/Flood boundary. This suggests that much, if not all, of the Precambrian sedimentary rocks and some associated igneous and metamorphic rocks are from the very early Flood.

## Impacts are a major mechanism for large arcs

Along with other possible mechanisms, large arcuate structures can be formed by meteorite or comet impacts. The rims of impact structures are circular to arcuate, depending upon how much post-impact change has occurred. If the impactor hit at a low angle to the horizon, the crater shape would be elliptical. Where the solid bodies in the solar system are not resurfaced by lava or debris, there are thousands of circular and arcuate rims (figures 1 and 2). Arcs from impacts would have formed by upward and outward thrusting of rock, or an outward vergence.<sup>1</sup> Vergence is the direction the thrust moves.

## Impacts did occur on Earth

Considering the number of extraterrestrial impact craters, it is not a stretch to think that the earth experienced numerous impacts. But those features are rare on Earth. According to uniformitarian geologists, there have been 200 impacts on Earth as of 2021, ranging from the Paleoproterozoic, 2.5 to 1.6 Ga, to the Holocene.<sup>2,3</sup> Of these, about 30 are Precambrian impacts, which are as old as 2.4 Ga,<sup>4</sup> including the Vredefort impact (figure 3), 250 km in diameter<sup>5</sup> and dated about 2 Ga, and the Sudbury impact (figure 4), 200 km in diameter<sup>6</sup> and dated at 1.85 Ga. Since the Vredefort impact is believed to have undergone 9 km of erosion and the Sudbury, 5 km, these structures must be deep crustal remnants.<sup>7</sup> These Precambrian impacts were significantly larger than the best-known impact on Earth, the Chicxulub impact.

## The Chicxulub impact

The Chicxulub impact is centred on the north shore of the Yucatán Peninsula of southern Mexico (figure 5). It is dated ‘very late Cretaceous’, and many scientists believe it was the extinction event for the dinosaurs. It was relatively large and resulted in a multiple-ringed crater with the outer ring believed to be about 180–200 km.<sup>8,9</sup> The impactor was estimated to be about 10 km in diameter (figure 6) and is considered the best representation of an impact crater on Earth. The Chicxulub impact occurred during the Flood and would have caused ‘impact winter’ for 3–15 years or more and helped to jump start the Ice Age.<sup>10</sup>

Clarey is sceptical whether Chicxulub was an impact because it lacks important diagnostic signatures; he thinks the structures could have been volcanic.<sup>11,12</sup> I agree that the Chicxulub impact is problematic, especially in terms of: its exact size; the lack of an iridium (Ir) anomaly; and relating the impact to a tsunami, the K/Pg boundary, and the extinction of the dinosaurs.<sup>13</sup> Chicxulub has little iridium and exhibits a small amount of expected melted and broken up rock.

Nevertheless, it has a fairly circular gravity anomaly with a possible peak ring of broken granite and a possible annular low. It also shows up to several hundred metres of suevite, shocked quartz, coesite, a little pseudotachylite, a small amount of melt, and a few shatter cones (figure 7).<sup>14</sup> Suevite is a broken-up rock deposit that contains deformed melt rock clasts and glass. Coesite is a high-pressure palynomorph of quartz. Pseudotachylite is a special type of broken up rock that contains some frictional melt and is caused by

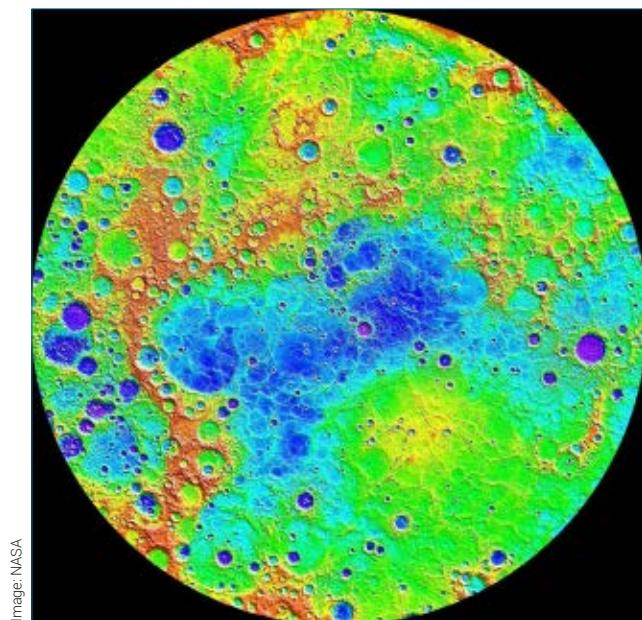


Image: NASA

**Figure 1.** Colour-enhanced topographic image of Mercury's northern hemisphere from the Messenger spacecraft, showing numerous impact craters

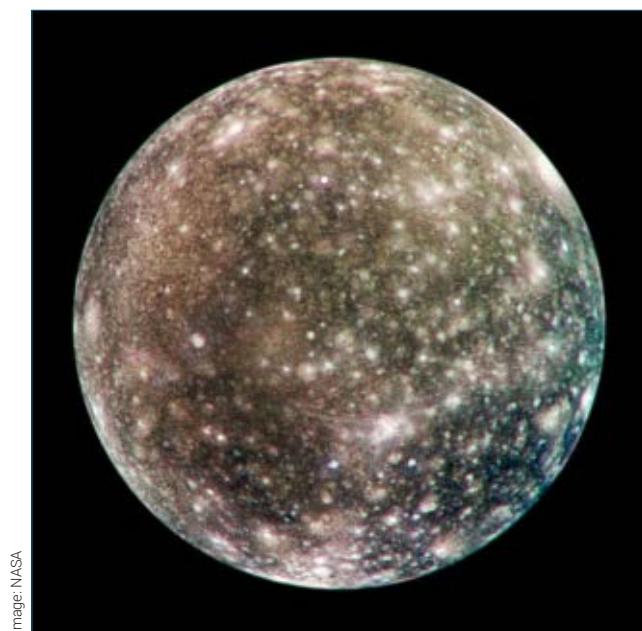


Image: NASA

**Figure 2.** Jupiter's moon, Callisto, showing numerous impact craters

catastrophic faulting, but it is difficult to distinguish from cataclasite. There were 130 m of suevite encountered in a new drill hole into the claimed peak ring structure.<sup>15</sup> Shatter cones are cone-shaped striated rocks associated with meteorite impacts, but the exact formation mechanism is unknown. Researchers recently found shocked zircon crystals, called ‘reidite’, associated with the M0077A borehole into the peak

ring structure.<sup>16,17</sup> Reidite is associated with other impact structures and is considered the only terrestrial mineral diagnostic of an impact.<sup>18,19</sup>

When all of these impact features are found together in one place, and realizing that shatter cones (see below) are associated with impacts, it seems that the Chicxulub feature represents a true Flood impact. As a detailed analysis of the Chicxulub impact shows, impacts during the Flood do not preserve pristine impact evidence because of tectonics, volcanism, erosion, and deposition. These subsequent Flood features can erode much of the evidence and distort the original impact features.

### A rough estimate of the number of ‘possible’ impact features

There are many impact craters on all the solid bodies in our solar system. They may be obscured by lava flows or debris. The number suggests that the earth has been struck by more than 200 impactors. Using the moon as an analogue, Spencer and I calculated that tens of thousands of impacts, leaving craters greater than 30 km, have struck the earth.<sup>20,21</sup> But we concluded that there had been far fewer.

It would be valuable to know the true number, since it would tell us more about the Flood and its boundaries. We can set the low end at the 200 recognized impacts, but many ‘possible’ impacts are probably real. Possible impacts can be identified by their arcuate to circular shape or by their subsurface seismic profile.

The *official* diagnostic criteria are too restrictive. French and Koeberl list four main diagnostic criteria: (1) shatter cones; (2) planar deformation features, such as shock metamorphic features in quartz (figure 8); (3) direct evidence, such as pieces of the impactor, tektites, or spherule layers; and (4) high-pressure/high-temperature minerals.<sup>22,23</sup> Tektites are millimetre- to centimetre-size spherules composed of black, green, brown, or grey natural glass formed from terrestrial debris ejected during meteorite impacts (figure 9). Most of the time, scientists do not know the location of the impact that caused the tektites, which can sometimes be found over wide areas called ‘strewn fields’. These four features have been used for a long time as the only proof of an impact. Morphology is given less weight.

However, these four criteria are ephemeral features that could easily be destroyed or remain undiscovered in both a uniformitarian model and the Flood model. Processes such as tectonism, volcanism, erosion, and deposition could have eradicated evidence. That is probably why there are more possible than confirmed impacts. These criteria alone do not identify all impacts, especially if they are buried:

“Although these criteria have been selected because they are unique physical products of bolide impact, strict adherence to these criteria means that we cannot positively identify buried astroblemes that are

tomographically imaged on three-dimensional seismic data, but are undrilled.”<sup>24</sup>

Possible candidates were assessed in an article on impacts in Africa. Some will prove to be impacts and some will not. There are 19 confirmed and 40 proposed sites; the latter being more than twice the confirmed sites.<sup>25</sup> I suggest that half of the possible impacts are true impacts. Thus, there would be about 19 more impact sites in Africa. If we apply this doubling ratio, the total will rise from 200 to about 400.

### Huge Archean impacts

There is a surprising and controversial recent discovery of 17 spherule layers in Archean (older than 2.5 Ga) sedimentary rocks in Western Australia and South Africa. The spherules are 0.1–4 mm in diameter and form layers ranging from 0.4–70 cm thick. The layers occur within volcanic, volcanioclastic, and sedimentary rocks many kilometres thick and have been dated at between 3.47 and 2.49 Ga.<sup>26</sup> The strongest evidence that they are from impacts is the enrichment of the platinum group, including Ir.<sup>27</sup> Koeberl *et al.* were once skeptical that they were from impacts because they are so close together stratigraphically that there would have been too many impacts in a few million years. So, they leaned toward a terrestrial origin. But two of the authors changed their minds.<sup>28</sup>

Chromium isotopes also indicate an impact origin,<sup>29</sup> though some are still skeptical because they cannot find the crater or shocked minerals, although no other explanation is likely.<sup>30</sup> Moreover, a crater and shocked minerals could easily be destroyed afterwards—both in secular and biblical history. Recently, shocked high-pressure rutile ( $TiO_2$ -II) has since been found within the spherules.<sup>26</sup>

The scientists claim that the bolides were 10–100 km in diameter!<sup>31</sup> A 10-km impactor would produce a crater about 150 km in diameter, about the size of Chicxulub. Larger impactors would result in gigantic craters and devastation. Some of the spherule layers are within banded iron formations (BIFs), suggesting a possible connection.

### Impact basins

Some cratonic basins look like craters. In addition, they show very thick sedimentary strata, rapid formation as indicated by little deformation during deposition, thinned crust with a raised Moho, and higher density crust.<sup>32</sup> Some cratonic basins have been uplifted, deformed, and had their top eroded, such as the Belt Basin in western Montana, northern and central Idaho, eastern Washington, and adjacent Canada. Many cratonic basins are large but are not included in even the ‘possible impacts’ category. But uniformitarian scientists do not know the origin of cratonic basins and why they subsided. It could be that such an origin is too catastrophic for uniformitarians.

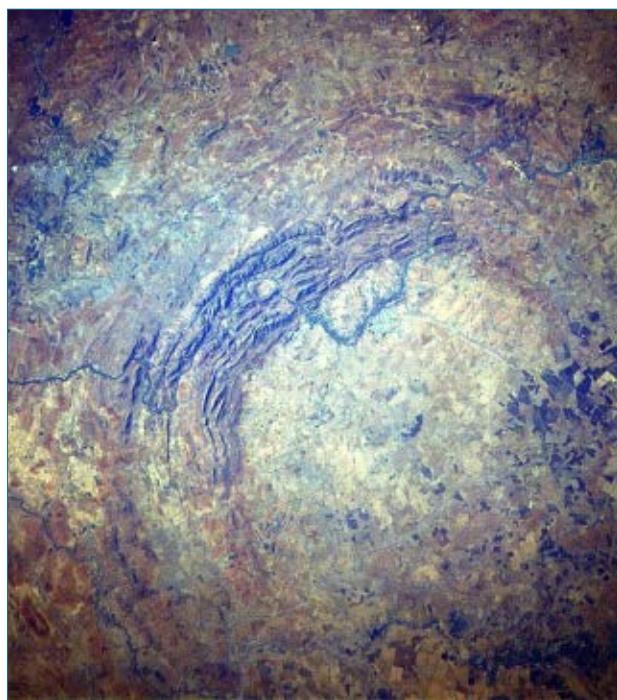


Image: NASA

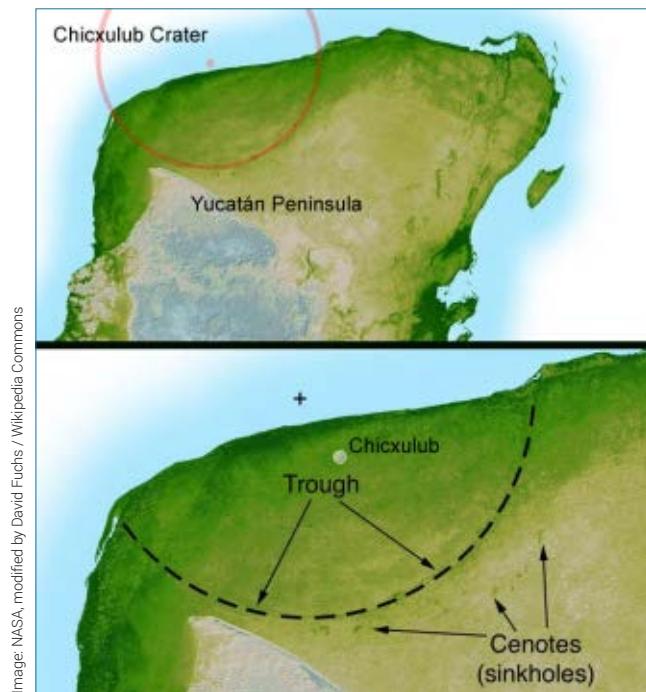
**Figure 3.** The upturned central portion of the Vredefort impact structures



Image: NASA (modified)

**Figure 4.** The almond-shaped Sudbury impact melt structure, southern Ontario, Canada

A new survey estimates that there are 764 basins.<sup>33</sup> A large proportion of these basins result from non-impact mechanisms, such as strike-slip, foreland, forearc, and fold and thrust basins. There are 66 cratonic basins not included as even possible impact candidates. Most are generally saucer shaped. Some of the non-cratonic basins, such as the 150 passive margin basins, 75 backarc basins, and 130



**Figure 5.** Shaded relief map of Mexico's Yucatán Peninsula showing estimated location and diameter of the Chicxulub impact. Numerous sinkholes cluster around the southern boundary of the impact structure.



**Figure 6.** Artistic rendition of the Chicxulub impactor striking ancient Earth

rift basins, could be caused by impacts, later distorted by subsequent geological processes, like the elliptical Sudbury structure (figure 4). Many marine backarc basins are caused by extension, but some could have an impact origin, such as the Alboran Sea Basin in the western Mediterranean Sea.<sup>34,35</sup> Some continental basins are called ‘backarc basins’, and some may be impact structures, such as the South Caspian Basin and the Western and Eastern Black Sea. If some of these have an impact origin, then it could push the number of continental impacts near 500. If the oceans are included, the number of impacts would have been many more.

### The largest known impacts would likely have devastated the earth

Even large ‘known’ impacts would have devastated large areas, as shown by computer models.<sup>36</sup> A 20-km asteroid would produce a crater the size of the Vredefort and Sudbury impacts. Such an impact would emit severe thermal radiation up to 1,000 km away. At 1,800 km, it would cause second degree burns and ignite deciduous foliage. At 2,000 km, it would cause no effect. A 30-km asteroid would produce a crater about 300 km in diameter, about the size of the smallest cratonic basins, and would ignite most life up to 2,000 km away. If the Belt Basin (~500 km) is an impact structure,<sup>37</sup> its asteroid would have been 50 km in diameter and would have ignited everything within 2,500 km. Larger impact basins would require a wider area of devastation.

Impacting should be a prominent mechanism for any Flood model. However, some Flood geologists have not addressed them.<sup>12,38</sup>

### Impacts during the Flood

Because of the potential devastation, I place most within the Flood, except for about 30 small ones, such as Meteor Crater, that are likely post-Flood (figure 10). Precambrian impacts likely did not occur during the Creation Week<sup>38,39</sup> or between the Creation Week and the Flood.<sup>40</sup> Precambrian impacts suggest a lower Flood boundary in those areas.<sup>41</sup>

The Flood would have destroyed evidence of most impacts, but arcuate features might be remnants. Some secular scientists agree that the arc shape, either on the surface or from seismic profiles, indicates a remnant of an impact crater.<sup>42</sup>

Often, these arcuate features show thrusting from the centre. Since arcuate mountains along the rim are characteristic of major impact basins on the moon,<sup>43</sup> why would they not be so on the earth, too? These rims are often a combination of uplifted and thrusted rock,<sup>44</sup> sometimes overturned by the outward push. Overthrusting would be emphasized by erosion.

Therefore, it is possible that many of the large arc-shaped features on Earth were formed by impacts. The Archean spherule layers would have been caused by very early Flood impacts. However, with rapid sedimentation also taking place, the spherule layers might represent only a few impacts rather than the large number attributed by uniformitarian scientists, who place millions of years between each spherule layer.

### Three possible solutions

Why so few impact structures on Earth compared to other solar system bodies? I suggest three possible answers: (1) God protected Earth relative to the rest of the solar system;

(2) the inner solar system bodies were bombarded on Day 4 of Creation Week, while the earth was not; or (3) both. I initially favoured the first possibility.<sup>45</sup> God oversaw the Flood for His *exact* purpose. The Bible says that God sat “enthroned over the flood” (Psalm 29:10 ESV), started the Flood (Genesis 7), and ended the Flood by the mountains rising and the valleys sinking (Genesis 8; Psalm 104:6–9).<sup>46,47</sup> So, it makes sense that He would have modulated the number of impacts to accomplish His purposes. In this case, the impacts likely would have come from the solar system passing through a large volume of asteroids and/or comets.<sup>48</sup> Nonetheless, after studying the surface of Mars, I now believe the third option: both (1) and (2) are true.

The second option is called the ‘Day 4 Cratering Hypothesis’.<sup>49–51</sup> This proposes that the heavenly bodies were *made* from pre-existing material created on Day 1, and that during and/or soon after assembly on Day 4, small objects were still present which later impacted the planets and moons. The earth was not affected since it was created on Day 1. Faulkner further suggests that the highlands of the moon and all the bodies of the solar system are the result of this Day 4 cratering, while the large basins around 1,000 km in diameter on the near side of the moon that are filled with basalt lava, the maria, were formed during the Flood by a narrow, intense swarm of very large asteroids travelling on parallel paths. Faulkner believes these asteroids only impacted the earth and moon.

The asymmetric distribution of the large craters on the near side of the moon (figure 11) suggests that the bombardment predominantly lasted for just days.<sup>52</sup> If the impacts took more than a month, large basins, assuming that they occurred during the Flood, would have been more random as the moon rotated.

After initially rejecting the Day 4 Hypothesis,<sup>53</sup> Spencer now believes it is true.<sup>54</sup> I believe the Day 4 Cratering Hypothesis because there was once a strong magnetic field on Mars that resulted in positive and negative remnant anomalies about 10–20 times stronger than on Earth,<sup>55,56</sup> which line up in an east–west direction (figure 12). They are unlike those on Earth and are about 100 km wide and up to 2,000 km long; they likely do not indicate plate tectonics on Mars, although some researchers have flirted with the idea.<sup>57,58</sup> They are found mostly in the southern highlands and most of the abundant small-to-medium-sized craters are part of the magnetic anomalies. The magnetic field did *not* remagnetize the large impact basins; large volcanic areas, such as the Tharsis rise; Valles Marineris; and much of the northern lowlands. The large impacts mostly destroyed the remnant magnetization, and the crust was not remagnetized because the magnetic field had already decayed: “Magnetic disruption near large impact craters such as Hellas and Argyre establishes that magnetization came before the impacts”.<sup>59</sup> The shock of the impacts demagnetized the crust.<sup>60</sup> The



Image: JM Gastonguay, Wikipedia Commons / CC BY SA 4.0

**Figure 7.** Shatter cone developed in fine-grained limestone from the Charlevoix crater, Québec, Canada, Collection of the Observatoire de l’Astroblème de Charlevoix

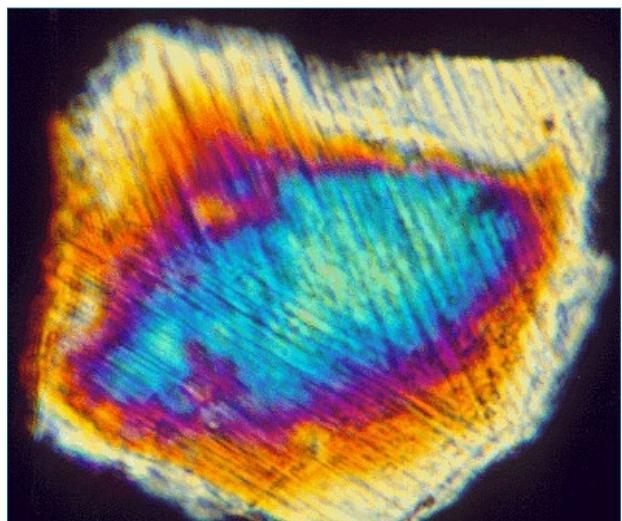


Image: Glen A. Izett, Wikipedia Commons / PD

**Figure 8.** Sand-sized quartz grain (0.13 mm) from the USGS-NASA Langley core showing two well-developed, intersecting sets of shock lamellae produced by the late Eocene Chesapeake Bay bolide impact



Image: Broken Imagery, Wikipedia Commons / CC BY SA 3.0

**Figure 9.** The two common shapes of tektites, dumbbell and teardrop, that resulted from an impact

Image: Shane Torgerson, Wikipedia Commons / CC BY 3.0



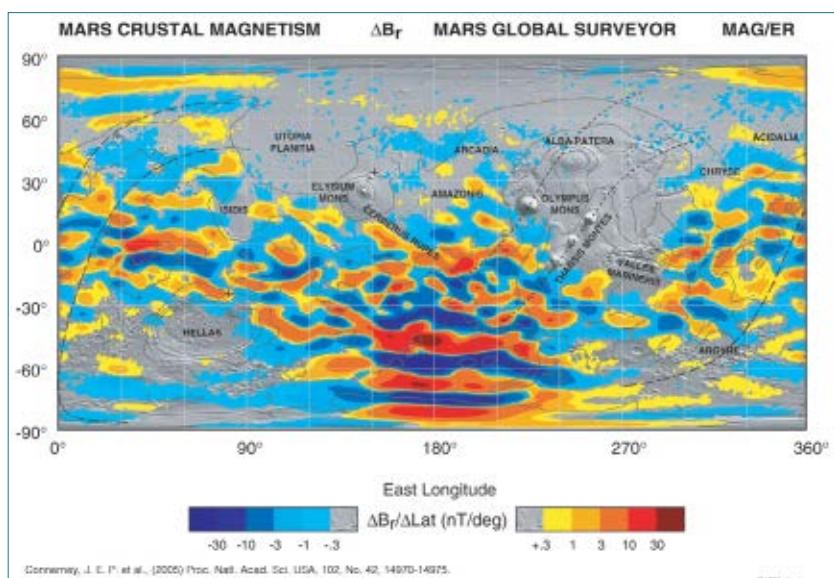
**Figure 10.** Aerial view of Arizona's Meteor crater

Image: Gregory H Revera, Wikipedia Commons / CC BY SA 3.0



**Figure 11.** The near side of the moon

Image: NASA



**Figure 12.** Map of the magnetic field of Mars observed by the Mars Global Surveyor satellite at a 400 km altitude. Red and blue stripes represent magnetic fields with opposite directions. Darker hues represent more intense magnetic fields. To show the location of the magnetic stripes on Mars, the map is superimposed on a topography relief map from the Mars Observer Laser Altimeter instrument.

volcanic regions would be expected to thermally demagnetize the area, but the magnetization did not recover later.<sup>61</sup>

These observations imply that the bombardment that created the southern highlands was very early in Mars history while the magnetic field was strong. The larger impacts came later when the magnetic field was either weak or had disappeared.

The half-life for the decay of Mars' magnetic field from an electromagnetic current within the core is 308 years.<sup>62</sup> So, by the time of the Flood—about 1,600 years after creation—Mars' magnetic field would have been very weak. Thus, the large impacts along with some small-to-medium-sized impacts likely can be placed within the Flood. Volcanism on Mars can also be placed during the Flood, suggesting a causal relationship between impacts and volcanism. Faulkner had the Flood impacts affecting only the earth and moon, but they must also have included Mars. It could be that other solar system bodies also received large impacts at this time.

However, Earth does not exhibit similar large impact basins like those on the moon and Mars, which is why I believe that God protected the earth from most of the large impactors while letting a smaller number of the medium to small impactors strike the earth. Some small to medium-sized impacts on Mars were also not magnetized, which would imply that they occurred when the large impactors struck during the Flood. Impact specialist Wayne Spencer once believed this, and probably still does:

“But whether we place impacts in Creation Week or at some other time, it seems inescapable that some unknown factor reduced the effects of impacts on the earth. Some sort of intelligently directed bombardment that limited objects' trajectories could also be a possibility, but this is very close to Faulkner's hypothesis also. It is very difficult to imagine some natural physical effect that would so dramatically reduce the number of impacts on earth. Thus some degree of supernatural protection of earth from impacts seems to be a necessity, regardless of when they took place. If supernatural protection of earth is a possibility, this in turn opens up the possibility of impacts in the solar system at some time prior to the Flood.”<sup>63</sup>

## Impacts could have caused the Flood

Even 500 continental impacts would have supplied a lot of energy during the Flood. It is even possible that they caused the Flood. Many details of an impact origin for the Flood need to be worked out. Some creation scientists suggest that impacts could have initiated Catastrophic Plate Tectonics,<sup>21</sup> which is also possible.

## Impacts help to define the pre-Flood/Flood boundary

If impacts caused the Flood, Archean and early Proterozoic impacts can help define the location of the pre-Flood/Flood boundary, assuming the geological dates are a relative timescale. Based on hundreds of metres of volcanic and sedimentary rocks, and eight<sup>64</sup> nine, or more<sup>65</sup> Archean spherule layers, more than nine impacts could have occurred at this time. Since it is believed the spherules fell from the atmosphere in marine waters, there could have been fewer than nine within biblical Earth history with rapid sedimentation.

Where would such impacts be placed within biblical Earth history? They are unlikely to have occurred during Creation Week, contrary to the beliefs of Dickens and Snelling.<sup>39</sup> If they occurred during Creation Week, it had to have been before the creation of vegetation on Day 3. However, celestial objects seem to be the province of Day 4. Moreover, it would be very difficult to place them between the creation and the Flood,<sup>40</sup> since the spherule layers are found in volcanic and sedimentary rocks over 10 km thick. This implies huge catastrophic action with very large impacts that would likely devastate large parts of the earth.

Therefore, these impacts are better placed in the very early Flood.<sup>46</sup> This deduction is supported by other features of the sedimentary rocks, such as raindrop imprints, black shale, carbonates, and phosphorites, which pass from the Precambrian into the Paleozoic with little or no change.<sup>67</sup> Raindrop imprints are found even in late Archean rocks. Thus, it is possible that all Precambrian sedimentary rocks, even as old as Archean, are from the Flood. Moreover, since some spherule layers are within BIFs, it can be implied that these enigmatic sedimentary rocks are also from the Flood. BIFs could be a geochemical product of the fountains of the great deep.<sup>68</sup>

## Conclusions

Impacts are well known to form large arcs. With 200 impacts confirmed on Earth, more are likely. Based on the large number of proposed impacts, Archean spherule layers, and basins, I estimate the total number at about 500 on the continents. The larger ones were so devastating that they must have impacted during the Flood. There are relatively few

impacts on Earth compared to other solid solar system bodies because practically all these impacts hit all but Earth on Day 4, and God likely modulated the number that impacted Earth during the Flood. The largest impacts bring up the possibility that they may have caused the Flood. This is a hypothesis that needs development. The impacts also indicate that most, if not all, Precambrian sedimentary rocks, and some igneous and metamorphic rocks, formed during the very early Flood.

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# Mendelian speciation: part 1—what is the abundant source of significant biodiversity?

Nigel E.A. Crompton, Thomas Sprague, Royal Truman, and Reinhard Junker

Information in the genome required to produce new species (or phenotypes) must either mutate into existence or be already encoded as alternate genetic programs. Mendel demonstrated the latter to be correct. Three fundamental Mendelian principles explain how new species arise rapidly: latent information, exponential trait combinations, and loss of heterozygosity; and these neither require any new genes nor a multitude of mutations. Latent information can remain unexpressed through three mechanisms: dominance, epistasis and transposition. Upon suitable mating, latent traits can become visible in the progeny. Pre-existing genetic programs encoding alternative traits, shuffled at meiosis and maintained by reproductive isolation, is the only observed and empirically tested source of speciation in eukaryotes. Mendelian speciation can produce significant multi-feature phenotype change; a distinction typically displayed even by close species. It can achieve this rapidly, obviating the need for very long evolutionary time.

For many decades creation scientists have reflected on how so many species with so much biological variety could have arisen quickly; in particular, among the animals which descended from Noah's Ark. Old-Earth creationists have been heavily influenced by evolutionist beliefs on how new traits (and species) arise, and these mechanisms seem to require millions of years. The mistake has been to assume Adam and Eve (along with other organisms) were created without internal genetic diversity, their phenotype fixed, and endless random mutations were needed to produce change.<sup>1</sup>

As Carter pointed out, the notion of ‘the fixity of species’ is a relic of Aristotle’s influence, which Darwin wrongly assumed the Bible taught.<sup>2</sup> Young Earth Creationists (YECs) agree that “organisms are designed to vary” as Williams phrased it.<sup>3</sup> This consensus view was well-expressed by YEC researcher Borger, who wrote, “life on Earth thrived due to frontloaded baranomes—pluripotent, undifferentiated genomes with an intrinsic ability for rapid adaptation and speciation.”<sup>4–7</sup>

In a series of papers, Carter documented various mechanisms YEC scientists have been evaluating for the origin of genetic variability.<sup>2,8,9</sup> These include: distinct germ cells in sexually reproducing, created organisms; a variety of individual animals within a created ‘kind’; heterozygous alleles; recombination to split alleles in the new chromosomes formed; retrotransposons which modified gene expression; gene gain and loss (e.g. for bacteria); and various forms of epigenetic inheritance (which includes imprinting).

Williams noted that biological information, which guides all aspects of an organism’s life processes, must reflect the intention of the Creator. Species-level DNA-encoded differences can include point mutations, crossing over, indels, transpositions, jumping genes, and any other enzyme mediated process.<sup>3</sup>

In this 3-part series, we refer to some of the sources of biological diversity mentioned above. The short-coming in all of these is clearly *microspeciation*: cause DNA change in a fruit fly, it remains a fruit fly. However, speciation is typically far greater than this, involving the expression of *multiple significant traits simultaneously*. We examine how Mendel’s findings provide an explanation for such holistic genetic change, and how this can occur rapidly.<sup>10</sup>

## Mendel’s seminal insights: the most promising explanation for rapid speciation

Where does biodiversity come from? How can diversity arise within genetic families or basic types? Could new species have arisen quickly following the Genesis Flood? Gregor Mendel, famed for his laws of inheritance, discovered a solution whose significance has been underestimated. Observations of rapid speciation are strong indicators that speciation does not result from Darwin’s natural selection and mutations, but rather as a result of Mendel’s law of exponential trait combinations<sup>11</sup> employing pre-existing genetic programs.

The question of how speciation occurs, i.e. the splitting of one species into two or more daughter species, is one of the central questions in biology. Charles Darwin’s epoch-making work, *On the Origin of Species*, addresses this question explicitly in its title.<sup>12</sup>

According to the Modern Synthesis of Evolution, species are said to have diverged and fragmented by the gradual accumulation of many mutations; populations being separated geographically, and differential selection acting on the separated subpopulations. Eventually, over time, reproductive barriers are said to have arisen (genetic isolation). It also includes the possibility of gradual sympatric speciation. On

this basis, large periods of time for the formation of new species are claimed to be necessary. This is now mainstream evolutionary biology.

A contemporary of Darwin's, the Augustinian friar Gregor Mendel, considered the father of modern genetics, had a very different take on the origin of species. It is based on pre-existing diversity encoded in genetic programs which can produce speciation within a few generations; biological novelties do not need to arise via lengthy mutation-selection cycles.

Mendel's work provides a clear understanding for how species can appear within genetic families. Mendel's concept—Mendelian speciation—will be presented in this 3-part series and compared to the mainstream evolutionist

view. Crompton has drawn attention to this topic for many years,<sup>13–16</sup> directly communicating with members of the US creationist community, during the mid-2000s. Much of the content in this current series has also been discussed, since 2004,<sup>17</sup> during conferences sponsored by the German creation science organization Wort und Wissen.

### Where does the biological diversity in nature come from?

Why are lions and tigers similar and yet significantly different? Why are Red Admiral and Painted Lady butterflies similar and yet significantly different? Why are wolves relatively homogeneous as a species and yet dogs, their artificially bred offspring, represent such a plethora of different breeds? Why can some organisms produce a wide variety of new species when colonizing sea islands, yet others do not? Explanation of speciation must be able to go beyond limited biological change, restricted to traits or genes; and must encompass significant biological change, affecting many features of an organism.

Darwin was a passionate biologist and claimed that natural selection was the means by which new species arose. Many today believe he solved the mystery of speciation. Before Darwin, most scientists attributed biodiversity to divine agency, but afterwards the credit was given to natural selection. A fundamental shift in scientific thinking resulted which ignored any divine contribution and required eons of time. In fact, Darwin's premise was not correct. Selection, whether natural or through deliberate breeding is not the true mechanism that produces new characters or new species. Only after the phenotype of a novel species has appeared (i.e. after the origin of species) can natural selection act to favour the new phenotype, which should be fitter.

In 1905 de Vries (one of the fathers of mutation theory) recognized that

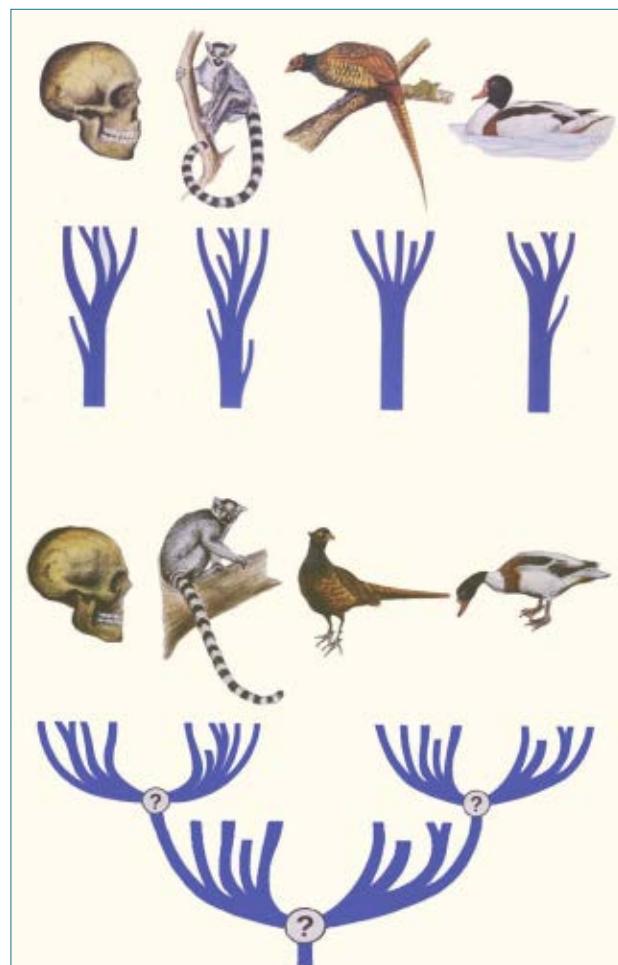
“... natural selection may explain the survival of the fittest, but it cannot explain the arrival of the fittest.”<sup>18</sup>

Professor Andreas Wagner at the University of Zurich used this insight to write a book, *Arrival of the Fittest*.<sup>19</sup> He noted correctly:

“And if we do not know what explains its arrival, then we do not understand the very origins of life’s diversity.”<sup>20</sup>

Remarkably, considering the subtitle of his book, *Solving Evolution’s Greatest Puzzle*, Wagner did not offer any new explanation for the origin of novel phenotypes either.<sup>21</sup>

Natural selection, it is claimed, produces *de novo* novelty but through use of nebulous and misleading phrases like, ‘caused by environmental pressures’ and ‘convergent evolution’.



**Figure 1.** *Cis*-evolution versus *trans*-evolution. Top: *Cis*-evolution. Each independent family is shaped like a tree, displaying *cis*-evolution. The branches (species) are kept apart by reproductive isolation, but may occasionally reunite by sporadic hybridization. Such diversification is proposed to result from pre-existing genetic programs and Mendelian speciation. Bottom: *Trans*-evolution. All families are claimed to be ancestrally linked, and these links are claimed to have arisen through mutations and selection. From Junker and Scherer with permission.<sup>23</sup>

## Single common ancestor or multiple independent lineages?

The eukaryotic world is extremely diverse, encompassing millions of species.<sup>22</sup> It could be interpreted as a monoarboreal single lineage tree of life or sylvan, characterized by a multi-lineage forest (see figure 1).

Both models assume an ancestral species, but they have very different views as to the ‘how’ new species arise and the magnitude of the changes. How species arise addresses what is arguably the most important question in biology: Are species fixed within certain limits beyond which they cannot change (leading to a forest-like phylogenetic pattern), or can species vary without limit (allowing all living things to have derived from a single organism)? It was a question discussed by Mendel.<sup>24</sup>

## Mendel's sidelined experiments

Gregor Mendel (figure 2) investigated seven *characters* of the garden pea, including seed colour, seed shape, flower colour, pod colour, pod shape, stem length, and flower position.<sup>10</sup> Each of these characters was represented by two *traits*; for instance, seed colour can be either yellow or green, and seed shape can be either round or wrinkled. (The three terms: trait, character, and phenotype, are crucial to a correct understanding of Mendelian speciation. They are explained in the glossary).

Mendel's publication provided an explanation for the rapid origin and vast number of new species.<sup>10,25</sup> But his groundbreaking discoveries had no influence until the significance of his work became recognized thanks to three independent articles in the March, April, and June 1900 editions of the *Report of the German Botanical Society*. The authors were de Vries,<sup>26</sup> Correns,<sup>27</sup> and Tschermak.<sup>28</sup>

Correns recognized the significance of Mendel's publication clearly:

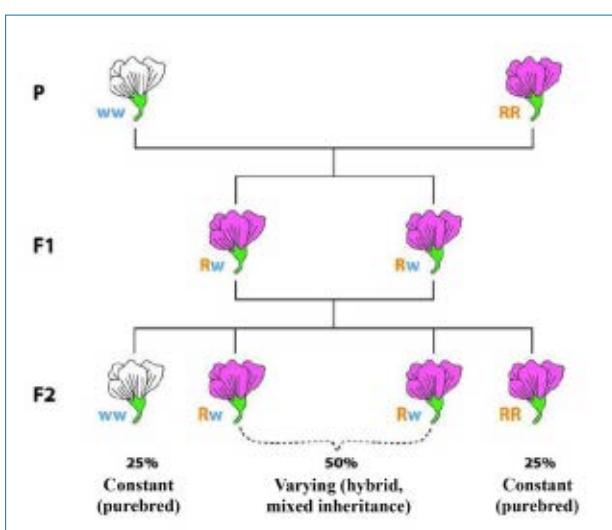
“It hardly needs to be said that this behaviour is of importance for the question of whether hybrids can become species.”<sup>27</sup>

Mendel had discovered the source of diversity in eukaryotic organisms. The underlying physiological process would later become known as meiotic recombination, and with this discovery Mendel had unravelled the mystery of the origin of (eukaryotic) species.

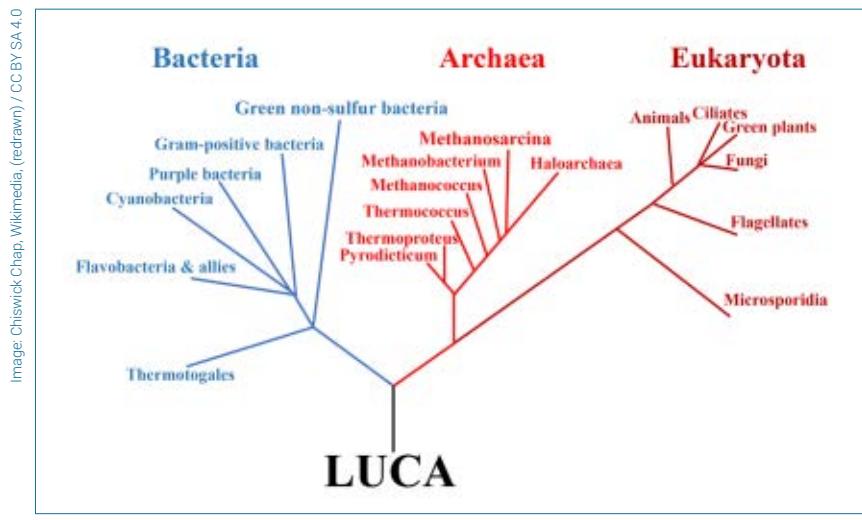
Mendel recognized the *Law of Exponential Trait Combinations* at least three times in his famous paper on plant hybrids.<sup>11</sup> It is the only proven mechanism able to generate (non-trivial) new species within eukaryotic families. Biology and genetics textbooks ascribe two, sometimes three, other laws to Mendel: the *uniformity rule*, *splitting rule* (figure 3), and *independence rule*, as discussed in the Appendix.



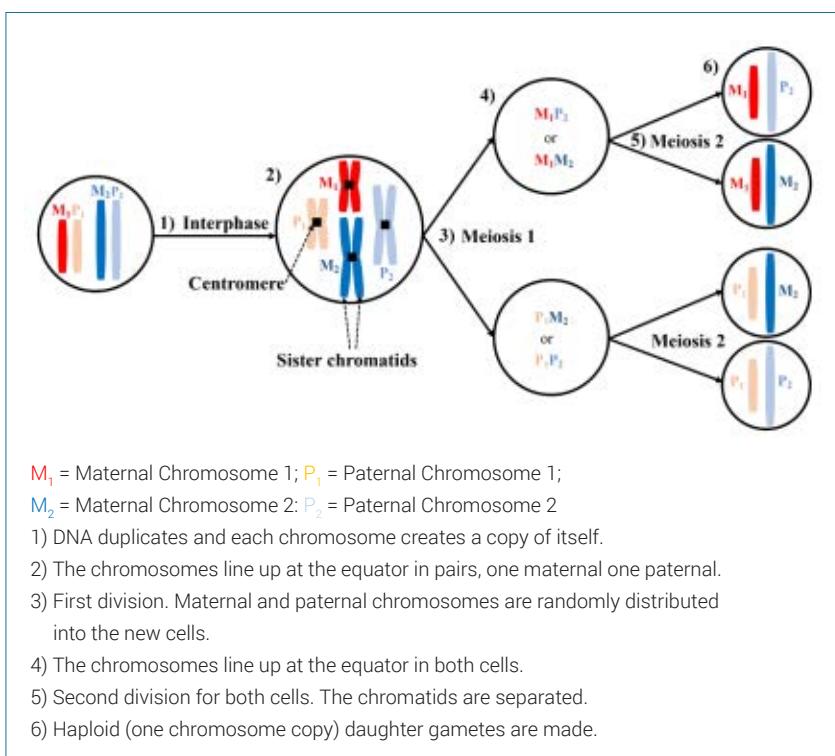
**Figure 2.** Gregor Johann Mendel (1822–1884), the father of modern genetics, was born in Heinzendorf, Schlesien (today Hynčice in the Czech Republic). He was an Augustinian friar (not a monk) in St. Thomas' Abbey, Brünn, Austria (now Brno, Czech Republic). He conducted his experiments with plant hybrids between 1856 and 1863, presented his findings at the Brünn Society for Natural Sciences in February and March of 1865, and published his famous paper in their proceedings journal in 1866.<sup>10</sup> (Courtesy of St. Thomas' Abbey, Brno)



**Figure 3.** Illustration of the uniformity rule (at generation F1) and the splitting rule (at generation F2) in monohybrid dominant-recessive inheritance. Below: difference between constant (homozygous, purebred) and varying (heterozygous, mixed inheritance) offspring.



**Figure 4.** High-level tree of life rooted on a Last Universal Common Ancestor (LUCA), according to Woese *et al.*<sup>31</sup>



**Figure 5.** During meiosis, gametes (sex cells) are formed. The gamete mother cells are diploid. They have two sets of DNA, one from the maternal and one from the paternal parent. After meiosis 1 at 4), both daughter cells inherit, in a random manner, one chromosome from each chromosome pair, each having two chromatids. After meiosis 2, the four gametes inherit those same chromosomes, but each now has one chromatid. The gametes are haploid and inherit just one set of chromosomes. During gamete formation, the DNA is recombined in segments, each segment being inherited either from the original maternal or the original paternal DNA. At prophase 1, chromosome segments; at metaphase 1, whole chromosomes are exchanged. For a more detailed explanation, see [Meiosis—Khan Academy](#). Exchange of DNA segments (cross-over) at prophase 1 is not displayed in the figure.<sup>33</sup> Figure by R. Truman. Original diagram based on [Meiosis: Its Stages—Study Mind](#).

Using current knowledge of molecular biology, we call these rules Mendel's Law of Segregation (rule 1 and 2) and Mendel's Law of Independent Assortment (rule 3). Mendel's research provided the evidence for these two laws, but he never formulated them explicitly. The second law is actually deficient; the possibility of gene linkage only realized later by geneticists.

Mendel demonstrated that combining independent alternate traits could produce an exponential number of phenotypes (different plants). This was pointed out in an excellent review by Ellis *et al.*, who noted that Mendel's emphasis was on speciation, the transformation of one species into another.<sup>29</sup> Mendel's Law of Exponential Trait Combinations confirms that much information is already encoded in genomes. This fact is sufficient to explain most of the diversity observed within eukaryotic families.

Darwin's *On the Origin of Species by Natural Selection* was published in 1859, while Mendel was simultaneously conducting his experiments (1854–1865). Mendel had a copy of the 1863 first German translation of Darwin's book and understood that Darwin was suggesting all life could have arisen from a single common ancestor.<sup>30</sup> A modern version of Darwin's view is shown in figure 4.<sup>31</sup>

Based on his results, and discussions with others involved in breeding plants, Mendel thought there were many independent lines of descent in nature. However, as a good scientist, he recognized the limited sample coverage of his experiments; mostly with the Garden Pea, *Pisum sativum*; a few with hybrids of two Common Bean varieties, *Phaseolus vulgaris* and *P. vulgaris nanus*; and a few with hybrids of two separate species, the Common and Runner Beans, *P. vulgaris* and *P. coccineus*; but was unable to interest others to experiment with other organisms. He was therefore cautious about overgeneralizing his results (the

cautionary approach being a good practice many origin-of-life researchers are encouraged to imitate).

### Fundamental principles in Mendelian speciation

Mendel's experiments on seven plant characters reveal three fundamental principles that together result in Mendelian speciation:

- I. Latent information
- II. The law of exponential trait combinations
- III. Loss of heterozygosity.

#### I. Latent information

Mendel deduced the presence of latent information during his experiments with hybrids when introducing the terms '*dominant*' and '*recessive*' expression.<sup>32</sup> He called a plant trait recessive if it was not expressed for a generation but remained potentially available to be expressed in subsequent generations.

As will be elaborated on in part 2 of this series, the genetic information is held in a latent state by at least three mechanisms:

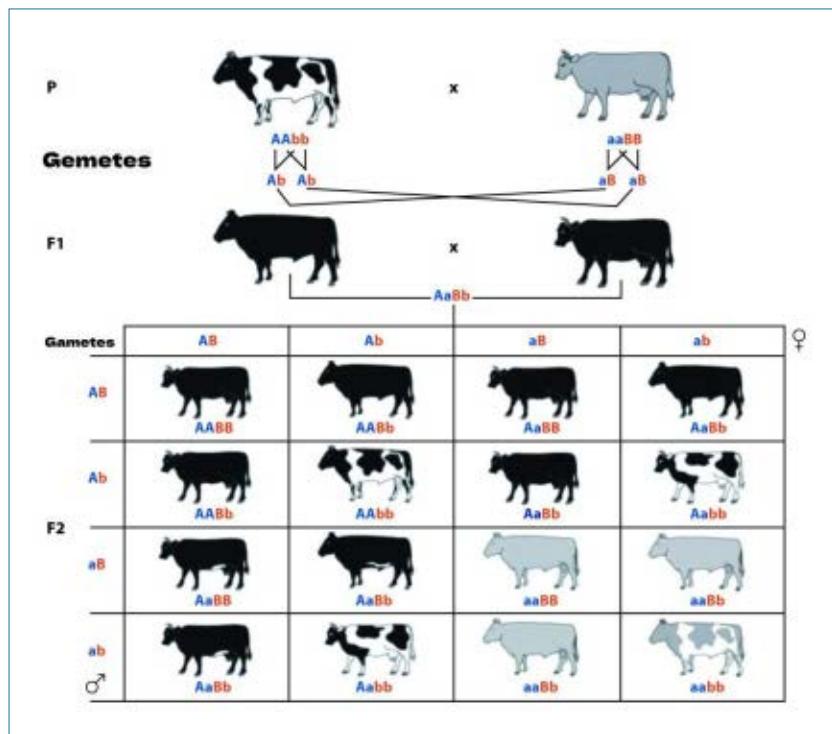
- dominance
- epistasis
- transposition.

#### II. The Law of Exponential Trait Combinations

Mendel's studies of plant hybrids revealed a satisfactory explanation for how novel trait combinations arise. The mechanism at work in eukaryotes is now known as meiotic recombination, as shown in figure 5.<sup>33</sup>

Pairs of the same chromosome (one paternal, one maternal) are called 'homologous chromosomes'. The Law of Independent Assortment states that during meiosis all genes are randomly distributed among the four daughter cells; see stage 6) of figure 5.

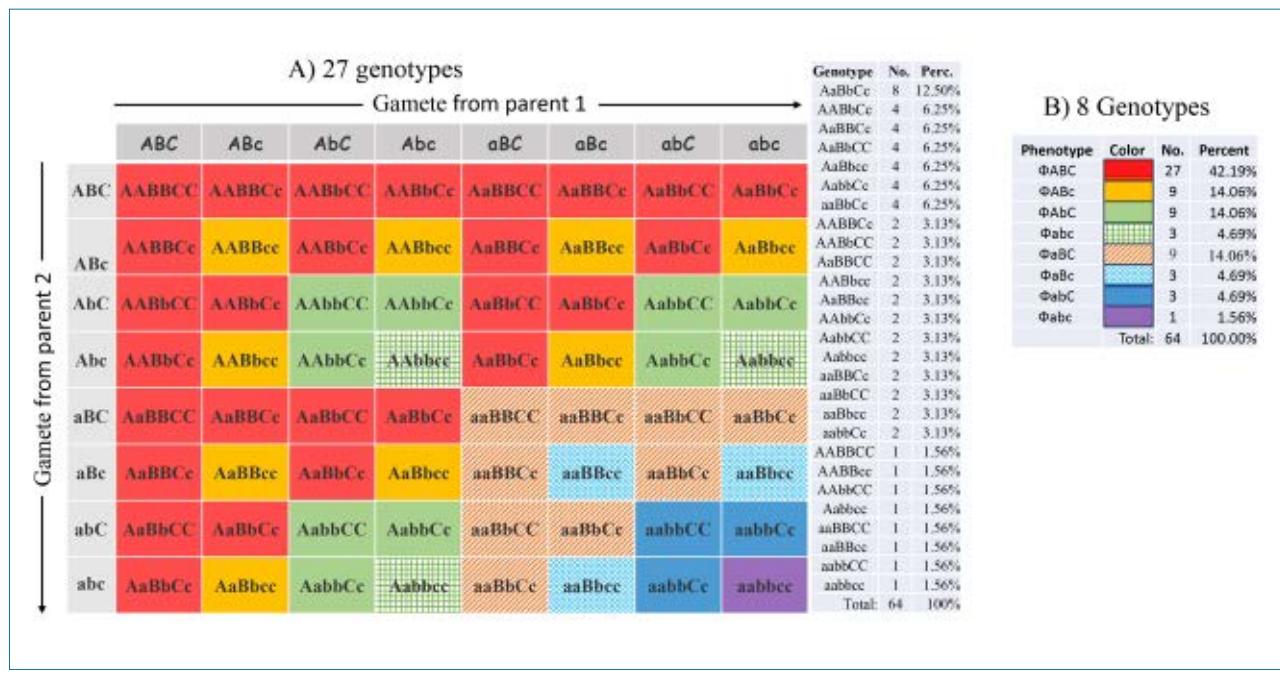
Meiosis will be discussed further in part 2 of this series. Non-meiotic organisms such as prokaryotes use other mechanisms to exchange genetic information. For example, plasmids and viruses provide a reservoir of genes that can be transferred to prokaryotes,<sup>34</sup> and antimicrobial resistance can be conferred by viral genes.<sup>35</sup> There are alternative methods to effectively transfer genes between prokaryotes.<sup>36</sup> However, eukaryotes undergo Mendelian speciation.



**Figure 6.** Illustration of the uniformity rule (at generation F1) and the splitting rule (at generation F2) for dihybrid (doubly heterozygous) inheritance. Single-colour (solid) is dominant over spotted; black is dominant over grey. In the F1 generation, the recessive traits (for grey and piebald) are hidden (latent).

Using the Law of Exponential Trait Combinations, Mendel was able to predict the expected ratio of genotypes in monohybrid, dihybrid, and trihybrid crosses. He discovered the 3:1 phenotype ratio of dominant to recessive trait expression (figure 3). But Mendel's research went even further. He recognized that the dominant phenotype could be either constant (homozygous) or varying (heterozygous). He showed that, when heterozygous, progeny could display dominant or recessive traits; but, when homozygous, progeny would only ever display that one trait. Today we understand this is because genes are present as two copies, called 'alleles' (one from each parent). If the alleles are identical (the gene is homozygous) the progeny can only inherit one allele and so can display only one trait; however, if the alleles differ (the gene is heterozygous), the progeny can display either of the traits, depending on which pair of alleles they inherited.

Mendel showed that the dihybrid genotype (two heterozygous genes) leads to 9 unique genotypes with a relative proportion of 1:1:1:2:2:2:4 (viewing a Punnett square from top left to bottom right, see figure 6, this ratio can be written 1:2:1:2:4:2:1:2:1) as shown in figure 6. In genetics textbooks, the ratio typically described is 9:3:3:1, referring to the phenotypes that are seen, because the genotypes are usually unseen.



**Figure 7.** Punnett square with three genes showing the possible outcomes of a trihybrid self-cross. None of these traits are linked. A) 27 different genotypes (letter combinations) can form. The 8 unique phenotypes are shown in different colours. B) The frequency of the 8 different phenotypes (f). Capital letters are used to designate a dominant allele, which dictates the phenotype.

The British biologist Reginald Punnett developed a compact method to determine the phenotype and genotype ratios in breeding experiments, known as the Punnett square. If drawn correctly, these squares display a high degree of internal symmetry that is revealed in the patterns of phenotype and genotype ratios. Figure 7 shows the Punnett square revealing the trihybrid (triply heterozygous) self-cross.<sup>37</sup>

Figure 7 shows the 8 ( $= 2^3$ ) distinct phenotypes which can form, and their expected frequencies. The 27 ( $= 3^3$ ) unique genotypes are also labelled. Note that there are as many unique gametes as unique phenotypes. The leading diagonal (top left to bottom right) reveals each of the 8 possible fixed phenotypes, which are the purely homozygous states; Mendel's 'constant' plants. All other genotypes are heterozygous; Mendel's 'varying' plants. The trailing diagonal (top right to bottom left) reveals the pan-heterozygous genotypes, which are able to generate any of the trait combinations. The pan-heterozygous plants possess the maximum phenotype information. Mendel's 'constant' and 'varying' plants are now referred to as 'pure-breeding' and 'hybrid' plants.

That two traits exist for each of the 3 characters explains the 8 ( $2^3$ ) different phenotypes and the 27 ( $3^3$ ) different genotypes observed by Mendel. Even though some phenotypes (trait combinations) look the same, Mendel

recognized that dominant traits could be either 'constant' or 'varying'; however, recessive traits are always 'constant'.

Mendel demonstrated experimentally that hybrid organisms followed his law of exponential trait combinations. Diversity increases exponentially with the number of characters. Plants possessing  $n$  (hybrid) characters can generate  $2^n$  different phenotypes and  $3^n$  different genotypes.<sup>38</sup> As a side-note,  $2n$  phenotypes arise when dominance is complete. If dominance is incomplete, intermediate phenotypes arise in the heterozygotes. The classic example of this is homozygous red and white carnations, and heterozygous pink carnations. In cases of co-dominance, double phenotypes arise in the heterozygotes. The classic example of this is homozygous blood groups A and B, and heterozygous blood group AB. In these circumstances more than  $2n$  different phenotypes can arise. However, during speciation, heterozygosity is typically lost, and these additional phenotypes will also be lost. Mendel examined seven varying characters and eventually observed all 128 ( $= 2^7$ ) unique phenotypes. Since his law is mathematically exponential, it readily explains the emergence of a multitude of phenotypes. Just 10 varying characters (heterozygous genes) can produce  $2^{10} > 1,000$  different homozygous phenotypes; 20 varying traits (heterozygous genes)  $2^{20} > 1,000,000$  different homozygous (pure-breeding) phenotypes. This is where the various species, and the diversity of nature, have their primary origin.

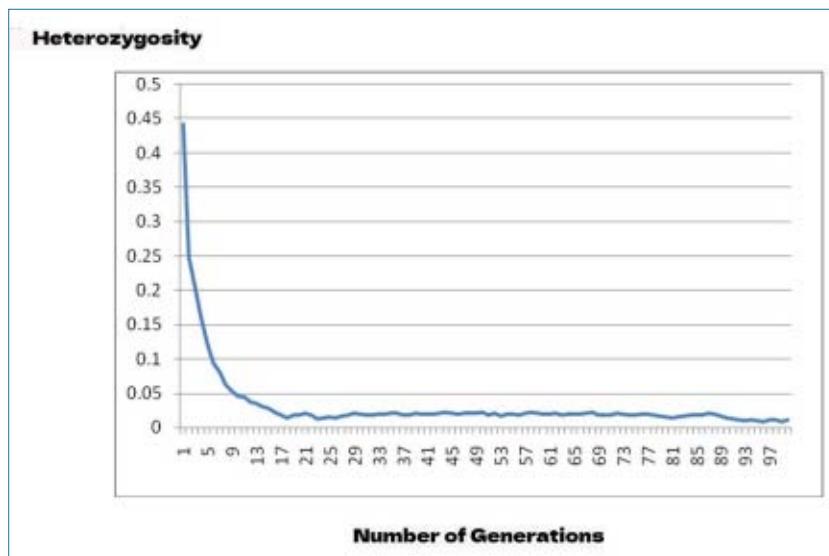
### III. Loss of heterozygosity

The third principle described by Mendel is a trend towards fixed, homozygous phenotypes, which is referred to as the loss of heterozygosity. This means that eventually only one trait of each character is displayed by all individuals in a subpopulation. This is crucial to the production of new species. Loss of heterozygosity's vital biological role in speciation often goes completely unappreciated, even by Mendel's biographers,<sup>39</sup> despite Mendel referring to the observation as a developmental law, 'Entwicklungsge setz'.

Mendel was familiar with the work of various other plant breeders such as German professors Kölreuter<sup>40</sup> and Gärtner.<sup>41</sup> They had observed that hybrids have a tendency to revert to the parent (pure-breeding) forms. Meiosis, shown in figure 5, is the reason for the loss of heterozygosity and for the well-documented reversion to pure breeds.

Suppose that trait *A* is dominant and trait *a* is recessive, and both parents carry both alleles. This can produce the combinations AA, Aa, aA, and aa in their offspring. Since traits Aa and aA are phenotypically equivalent, it leads to the expected genotypic ratio of 1:2:1. In this example, although both parents were heterozygous, only half of the children are. The other half are homozygous; either homozygous dominant or homozygous recessive. In the next generation, those 50% homozygous children give rise to only homozygous grandchildren; they are said to be 'fixed'. However, the 50% heterozygous children will once again give rise to half heterozygous grandchildren (25%) and to half homozygous grandchildren (25%). This is an unwavering feature of meiosis; each generation loses 50% of whatever heterozygosity the parents possessed, and the remaining children are homozygous. It is an important finding, first numerically explained by Mendel.<sup>42</sup>

If one starts with a situation where any individual can cross with any other individual, when left to naturally reproduce, every successive generation will retain the 1:2:1 genotype ratio; with its high proportion of heterozygotes. However, Mendel worked with Garden peas, which self-cross (self-fertilize). This is a crucial difference. In this situation, the ratio quickly changes. The starting, or P, generation are all hybrids; the F1 generation displays the genotype ratio 1:2:1; the F2 generation, the ratio 3:2:3; the F3 generation, the ratio 7:2:7; and the F5 generation, the ratio 15:2:15.

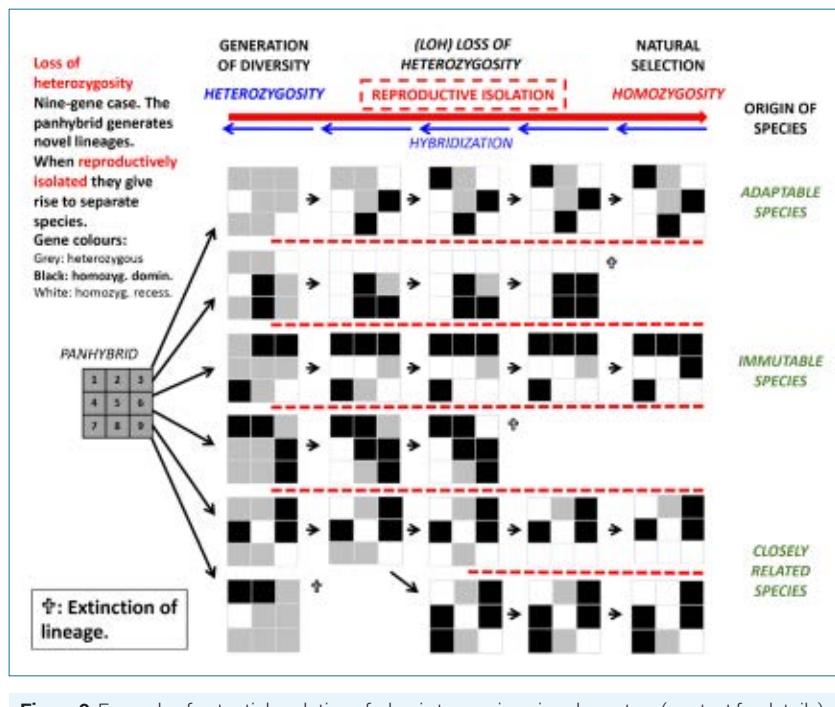


**Figure 8.** Proportion of heterozygous genes plotted against the number of generations in a typical population using a Monte Carlo simulation. Loss of heterozygosity, which corresponds to complete adaptive radiation of a genetic family with many new species and genera, took less than twenty generations. In this simulation, organisms were at liberty to occasionally interbreed, unlike Mendel's peas, which self-pollinated.

The outer two values are the homozygous-dominant and homozygous-recessive values, and the central value is for the heterozygotes. Within just a few generations the homozygous genotypes rule the roost. Of course, as with Mendel's peas, this assumes strict reproductive isolation.

The two-character (gene) case is much more complex, because there are increasingly more genotypes. The P generation begins with the dihybrid, AaBb. The F1 generation has the genotype ratio 1:2:1:2:4:2:1:2:1 and genotypes AABB, AABb, AAbb, AaBB, AaBb, Aabb, aaBB, aaBb, aabb. The F2 generation has the genotype ratio 9:6:9:6:4:6:9:6:9; the F3 generation, the genotype ratio 49:14:49:14:4:14:49:14:49; and the F4 generation, the genotype ratio 225:30:225:30:4:30:225:30:225. The '4' in the middle indicates the dihybrids, which get exponentially overwhelmed by the homozygotes (both the single homozygotes and especially the double homozygotes) at each successive generation. The two-gene self-cross overwhelms its hybrids faster than the single-gene self-cross. The three-gene self-cross is faster still. For a population to retain significant heterozygosity, it must have mechanisms in place to avoid self-crossing (reproductive isolation). Where this is not the case, populations quickly become homozygous, a situation that promotes speciation.

How quickly is heterozygosity lost in a population? Using an example based on one character (gene), Mendel predicted that within 10 generations a pan-heterozygous starting population (i.e. all genes fully heterozygous) would become



**Figure 9.** Example of potential evolution of a basic type using nine characters (see text for details). Graphic from N. Crompton.<sup>14</sup>

constant (homozygous), 50% dominant and 50% recessive; any hybrids would be reduced more than 1,000 fold.<sup>43</sup>

Buri studied 107 populations of (single gene) heterozygous fruit flies. After generation 6, populations appeared that were 100% homozygous.<sup>44</sup> By generation 19, almost all the populations were either 100% homozygous dominant or 100% homozygous recessive. Populations with more than one heterozygous gene show an equally rapid loss of heterozygosity.

Usually, species differ in more than one gene. Mendel discusses this in his paper.<sup>45</sup> He refers to workers with ‘sharp definitions’ of the term ‘species’, where even a single character difference is considered sufficient to confer species status, e.g. *P. quadratum* are pure-breeding garden peas with wrinkled seeds; *P. saccharatum* are pure-breeding garden peas with constricted pods; and *P. umbellatum* are pure-breeding garden peas with flower heads at the end of their stems. However, Mendel and most of his contemporaries preferred to refer to such groups as ‘varieties’.

The Oxford definition of a variety is “a group of individuals that differ distinctly from but can interbreed with other varieties of the same species. The characteristics of a variety are genetically inherited.”<sup>46</sup> Because Mendelian speciation employs meiosis, all the genes of an organism (not just one or a few) are involved; and this typically results in sister species varying in many characters.

Meiosis is a very different situation to that which results from the mechanisms usually proposed as causes

of speciation. Alternative mechanisms of genetic change based on mutations, or even transpositions, cause limited phenotypic change to organisms. If one mutates a fruit fly, it remains a fruit fly. If one triggers a transposition event in a peppered moth or a garden pea, you still have a peppered moth and a garden pea. No significant speciation has occurred. One’s organism simply displays a new trait or so. Mendelian speciation, however, is based on meiosis and therefore global genomic change. It can account for comprehensive phenotypic change, which readily accounts for new species.

We programmed a Monte Carlo mathematical model of populations based on 25 heterozygous genes and found that within about 19 generations almost all the genes had become either homozygous dominant or recessive, as shown in figure 8. The reason the curve levels off ‘above zero’ in the simulation

(after 20 generations) is that the organisms occasionally interbreed (not so with Mendel’s peas, which, after the first hybrid cross, only ever self-pollinate and which would quickly tend to zero).

The description above illustrates the fundamental processes at work. But natural populations are far more complex than the simplifying assumptions used for the model. For example: populations can be of different sizes; subpopulations may be only partially isolated; individuals carrying rare alleles can live beyond a single breeding cycle, passing it on through multiple generations. To more accurately model the richness of natural processes, we programmed the Monte Carlo simulation with several semi-isolated populations.

The model allows occasional random hybridization between groups (populations). The separated groups become, as expected, nearly pan-homozygous, but each with a different combination of alleles. The separate groups, therefore, form sources of new alleles for neighbouring groups whenever hybridization between the two occurs. Typically, these alleles persist briefly in the new population, but are lost again within a few breeding cycles. A more complete description of our models and their predictions is in a manuscript in preparation.

## Perspectives

The second paper of this three-part series takes a closer look at how genetic information is kept latent in

chromosomes. Dominance, epistasis, and transposition are all means of achieving this. A pan-heterozygous ancestor can hold a large pool of latent traits, sufficient to help produce all the existing species in a family of organisms. This completely circumvents the need for any new genes or for a vast number of random mutations.

The third paper of this three-part series takes a closer look at the crucial role of reproductive isolation in speciation. If progeny can freely mate among themselves, a single, highly variable species arises. However, if reproductive isolation interferes with this, and progeny are constrained in their mating; groups of unique, less variable, separate species arise. This mechanism of speciation can occur within tens of generations. Under appropriate conditions, the process gives rise to a species swarm, an adaptive radiation.

These processes provide a comprehensible and testable mechanism for rapid speciation based on pre-existing genetic programs, unlike Darwinian processes. Figure 9 illustrates how diversity can develop from a pan-heterozygous founding pair, in which all characters are initially heterozygous (i.e. both traits are present) under self-crossing conditions, and how different species arise.

In figure 9, population or species genotypes are represented as  $3 \times 3$  matrices. Each column of  $3 \times 3$  matrices represents a consecutive generation and each row an evolutionary lineage. Each cell within a matrix represents one character: black = homozygous dominant; grey = heterozygous; white = homozygous recessive. Each grey cell will express the dominant phenotype, but can pass on a recessive allele to the next generation.

The evolution of traits can be viewed as a stochastic process. Because subpopulations are reproductively isolated (dashed lines), homozygous characters (black or white) remain permanently fixed. The creation of alternative combinations of fixed traits (separate species) through the loss of heterozygosity is an ongoing process.

The loss of heterozygosity leads to unique, unvarying constellations of homozygous-dominant and recessive traits, thereby creating new species. Figure 9 indicates some populations (species) become extinct for various reasons (†). The last column represents extant populations or species. Most have retained some heterozygosity and therefore the potential for diversification. One species (3<sup>rd</sup> row) is fully homozygous. As such, it is an immutable species (lineage 3); like the cheetah or the northern elephant-seal. Only hybridization with a sister lineage (species) can restore heterozygosity, but with this comes the potential to form new species (see right-to-left pointing (blue) arrows).

Hybridization with other lineages has the potential to partially restore the original heterozygosity. In figure 9, some heterozygosity is still observed in the final generation of many of the lineages. A recent branching event is illustrated

in the two lowest lineages, and the offspring remain very similar. Hybridization between these two would restore the phenotype of their most recent common ancestor, but heterozygosity would be present only in characters 2, 7, and 8.

In the scenario shown in figure 9, no hybridization between existing lineages (populations or species) can restore the dominant trait of gene 9, or the recessive trait of gene 6, since the necessary genomic information has been lost from all of the various lineages.

## Concluding remarks

Mendel's experiments demonstrated how new phenotypes could become manifest, and quite rapidly, due to pre-existing genomic capabilities. Individual phenotypes are rapidly fixed in small, reproductively isolated subpopulations. New genes are not required for this process, nor multiple beneficial mutation events, nor long time periods.

These insights are profoundly relevant today to understand the genetic basis of rapid adaptability and adaptive radiations. For young-earth creationists, Mendelian speciation offers an empirically sound explanation for rapid speciation.

We propose that our Creator-God originally endowed basic kinds (genetic families) with genetic programs able to activate latent traits already encoded in the DNA relatively rapidly, through a variety of mechanisms, including loss of heterozygosity, but not all of the details of this process can be satisfactorily discussed, even in a three-part series.<sup>47</sup>

## Glossary

*Allele*: variant of the same gene, having a unique nucleotide sequence.

*Character*: particular feature of an organism, typically produced by one or more genes. Example: flower colour (the traits could then be, for example, purple or white).

*Dihybrid*: mixture of two characters. The individual is heterozygous at two different genes.

*Dominant*: An allele is dominant if it suppresses the trait caused by the other allele.

*Epistasis*: One (epistatic) gene masks the effects of a different (hypostatic) gene. Instead of the expected two traits, only one is observed. *Dominant epistasis* occurs when the dominant allele of the epistatic gene masks the effects of the hypostatic gene. *Recessive epistasis* occurs when the presence of both recessive alleles of the epistatic gene masks the effects of the hypostatic gene.

*Eukaryotes*: organisms with cells having a nucleus. They are normally capable of meiosis.

*Expression (gene expression)*: making usable the information encoded on a gene.

*Genetic family*: biological family whose member species possess different combinations of dominant and recessive traits, and the pre-existing genetic programs that code for them.

*Genome*: all of the DNA present in a cell.

*Genotype*: an organism's set of alleles at one, several, or all its genes.

*Heterozygous*: when different alleles of a gene are present in an organism.

*Homozygous*: when the same alleles of a gene are present in an organism.

*Hybrid*: of mixed parentage.

*Isolation*: separation of subpopulations and suppression of gene exchange outside the group.

*Latent*: hidden, concealed (here: in the genome). A trait or trait state is latent if it is genetically present but not phenotypically expressed.

*Meiosis*: the cellular process of chromosome exchange and inheritance by gametes (germ or sex cells).

*Monohybrid inheritance*: when a heritable character is controlled by a single gene.

*Mutation*: change in DNA, including: replacing nucleotides, deletions, insertions, and rearrangements.

*Phenotype*: the external appearance, relating to morphology, anatomy or physiology. It is used in two senses in this three-part series. 1. The sum of the observed traits. 2. The observed species, which is simply the sum of its traits.

*Pre-existing genetic program*: genetic information encoded in the chromosomes. The information codes for proteins, and regulation of their expression, which interact to produce the alternative traits of any given phenotypic character. The term 'pre-existing' refers to the fact that this information was present, prior to any speciation event; and it has been passed down through successive generations to the present.

*Recessive*: when the effect of a trait or an allele is suppressed by the presence of another (dominant) trait or allele.

*Recombination*: mixing of DNA segments or homologous chromosomes obtained from the parents during gamete formation.

*Speciation*: process by which a species splits into two daughter species.

*Trait*: the actual observed phenotype of a character. If the character of interest is flower position, then its traits might be terminal or axial. Typically, a trait is coded for by one specific allele of a gene.

*Trihybrid*: comprised of three characters. The individual is heterozygous at three different genes.

*Zygote*: the cell of eukaryotes formed after the fusion of an egg and sperm.

## Appendix: Various formulations of Mendel's Laws

Various laws have been attributed to Mendel which he did not actually formulate. Genetics textbooks in the English-speaking world generally have the following two (three) laws.

- Mendel's first law, *The Law of Segregation*, states that traits (or alleles) are randomly passed to the next generation due to meiosis.
- Mendel's second law, *The Law of Independent Assortment*, states that the genes are independently passed (sorted) to the next generation at meiosis. However, when multiple genes necessary to produce a character are physically nearby on the same chromosome, they could be 'linked' and thereby not truly independent.
- Mendel's third law, *The Law of Dominance*, is only rarely cited. It states that dominant traits (caused by alleles) mask (or hide) recessive traits.

German textbooks on genetics usually mention the following three rules or laws:

- Rule 1, the *uniformity rule* states that parents who are differently homozygous (e.g. one has aa and the other AA alleles) produce uniform heterozygous offspring.
- Rule 2, the *splitting rule*, states that parents who are equally heterozygous (e.g. Aa and Aa) split in the offspring both phenotypically and genotypically.
- Rule 3, the *independence rule*, corresponds to the Law of Independent Assortment, above.

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# Whales designed or evolved: part 1 – the fossils

Marc Surtees

Darwin suggested that whales might have descended from bear-like creatures, but until the 1980s there was no fossil evidence to support the evolution of whales from terrestrial mammals. The discovery of fossil ‘walking whales’ and other ‘archaeocetes’ has resulted in claims that the key steps in the transition, from fully terrestrial animals into obligate marine creatures via a series of amphibious intermediates, have been identified. Advocates of this evolutionary transition support their theories with various lines of evidence. This includes: 1) fossil archaeocetes (ancient whales); 2) hind-limb vestiges in modern whales; and 3) teeth buds and pseudogenes in baleen whales. Examination of the evidence shows that it is not always consistent with the claims and provides no viable theory to explain the appearance of the features which fit whales for life in the sea. An alternative way of handling the evidence is presented that is consistent with a suggested classification of the fossil archaeocetes and extant whales into basic types.

**W**hales, for example the blue whale shown in figure 1, are marine mammals which are extremely well designed for life in the sea. The list below gives some of the features which make these beautiful creatures so superbly fitted to life in the ocean:

- streamlined
- hairless
- blubber (for insulation)
- tail fluke (plus muscles and bones) for propulsion
- flippers for directional control
- heat exchanger circulatory system
- blowhole (muscles and nerves)
- specialized respiratory system (oxygen storage, lung collapse, heart rate suppression)
- salt elimination system
- echo location system (toothed whales)
- baleen (food extraction system)
- underwater birth and suckling
- specialized ear morphology.

These features provide considerable evidence of design, yet it has been claimed that “The origin of whales (order Cetacea) is one of the best-documented examples of macroevolutionary change in vertebrates”.<sup>1</sup> The fossil evidence which evolutionists point to includes more than 50 species of so-called ‘primitive whales’, which have been assigned to at least five families: Pakicetidae, Ambulocetidae, Remingtonocetidae, Protocetidae, and Basilosauridae.<sup>2,3</sup> According to evolutionary biologists, four-legged land creatures evolved all of the above features by the process of random mutations and natural selection over a period of about 10 Ma (million years).

Creation biologists have previously reviewed the evidence and concluded that it did not prove the claims of evolutionists. Woodmorappe, writing in 2002, showed

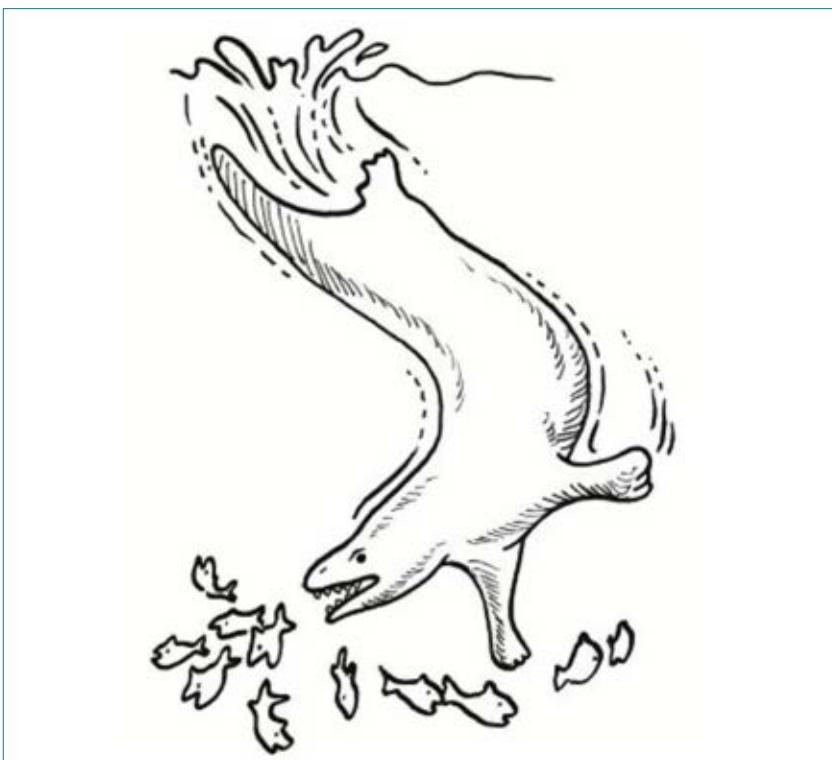
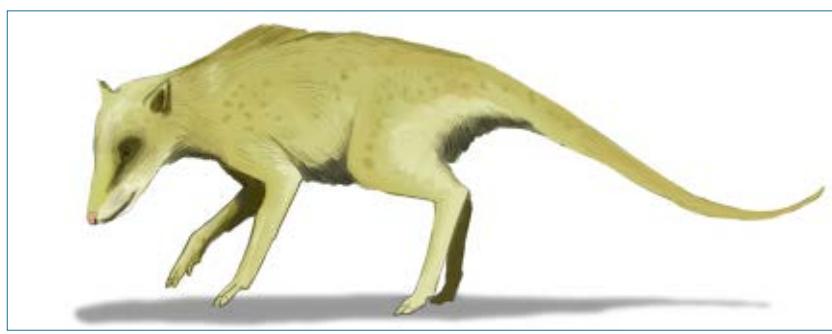
that the evidence available at the time was consistent with design.<sup>4</sup> Other more recent publications by creationists have reviewed newer evidence from evolutionists, as it became available, and found it lacking. This review attempts to bring together the currently available fossil evidence and comes to the same conclusion, which is that the evidence does not support evolution. One would expect that creation biologists would all agree, however some creation biologists have suggested that the ancestors of modern whales literally walked off the Ark and evolved into today’s modern whales and presumably dolphins.<sup>5,6</sup>

This first part of a two-part review will evaluate the reported fossil evidence and assess the validity of the claim that these fossils record the transition from terrestrial quadrupeds to fully marine-adapted creatures with flukes and flippers. The second part will look at some of the key design features which enable whales to live in the sea.

## Evolutionary ancestors?

One of the first reports of a ‘transitional’ fossil, which was claimed to be evidence that whales evolved from land animals, was published in 1981.<sup>7</sup> The authors described the partial skull of *Pakicetus* and were careful to point out that the post-cranial skeleton was unknown.

However, a later article, published in *Science*,<sup>8</sup> was accompanied by an artist’s reconstruction on the front cover of a creature diving into the sea to catch fish (figure 2). It was stated that *Pakicetus* provides the first direct evidence of an amphibious stage in the evolutionary transition of whales from land to sea. This was later found to be incorrect when more complete fossils were discovered, and it became clear that *Pakicetus* was fully terrestrial.<sup>9</sup>

**Figure 1.** Blue whale**Figure 2.** A drawing of the illustration of *Pakicetus* on the cover page of *Science* 220(4595) in which Gingerich et al.<sup>8</sup> described *Pakicetus*.**Figure 3.** Reconstruction of *Indohyus*, a small extinct artiodactyl known from fossils which evolutionists believe to be closely related to the ancestor of whales.

Another important fossil is that of *Indohyus* (figure 3), which lived in Asia. It was found in rocks described as middle Eocene, which evolutionists believe to be about 47 Ma old.<sup>3,10</sup> This was a small artiodactyl (hoofed animal, bearing weight equally on two toes), which is claimed to be closely related to the ancestor of whales because of the morphology of the bones of the middle ear.

The walls surrounding the inner ear cavity of most mammals are of a similar thickness all the way around. However, the internal wall of the inner ear cavity of extant whales is thicker than the external wall. This thickened wall, called the ‘involutrum’, is a distinctive feature shared by all cetaceans (whales and dolphins). The presence of the involucrum in all cetaceans is considered a major apomorphy (a trait which characterizes an ancestral species and its descendants) of cetaceans. Many evolutionists consider the involucrum to be an unequivocal diagnostic character for the cetaceans, including *Pakicetus*. Luo, writing in 1998, stated that “The involucrum marks the beginning of the development of pachystostosis (massiveness and hypertrophy) and pachyosclerosis (high density and heavy mineralisation) of the tympanic complex in cetaceans.”<sup>11</sup> In other words, they have thick, heavy ear bones.

It is also suggested, on the basis of the heavy bones and ratios of oxygen isotopes in the skeleton, that *Indohyus* was semi-aquatic and this is consistent with the presence of the involucrum, which is believed to be an adaptation to underwater hearing.<sup>12</sup>

Evolutionary biologists claim that there is a lot of other evidence to support the evolutionary account. For example, websites like that maintained by the University of California, Museum of Paleontology,<sup>13</sup> show an ‘evogram’ of a nice series of fossils as evidence that whales evolved from

creatures related to *Indohyus* and *Pakicetus*. This evogram presents a nice clean series of fossils which look increasingly whale-like as time goes on. There are a number of things which can be said about the information on this web site.

Firstly, and most surprising perhaps, is the statement in the opening paragraph that “In fact, none of the individual animals on the evogram is the direct ancestor of any other, as far as we know.” They refer to hypothetical ‘ancient relatives’. Once again, we find that evolutionists cannot produce any direct fossil ancestors for major groups of animals.

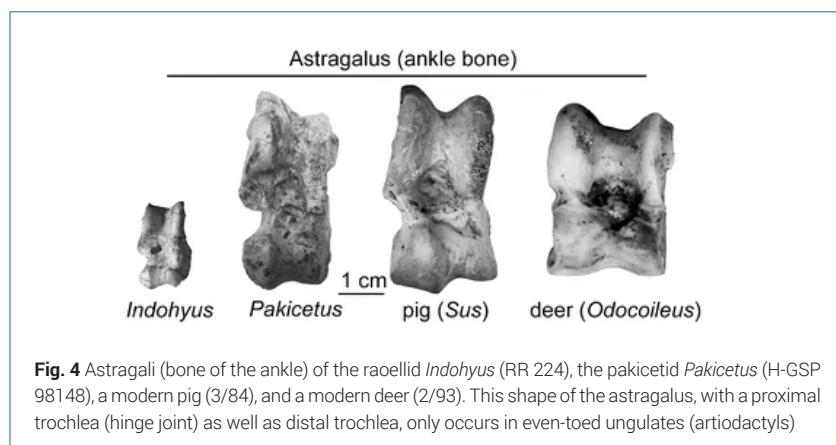
Secondly, they refer to a land creature such as *Pakicetus* as a whale, which is not a claim based on similar morphology or lifestyle, but only on the thick wall of the middle ear and robust ear bones.

Thirdly, there is a large gap between amphibious creatures like *Ambulocetus* and *Rodhocetus*, and the fully marine *Dorudon*, which has to be filled with some imaginative storytelling.

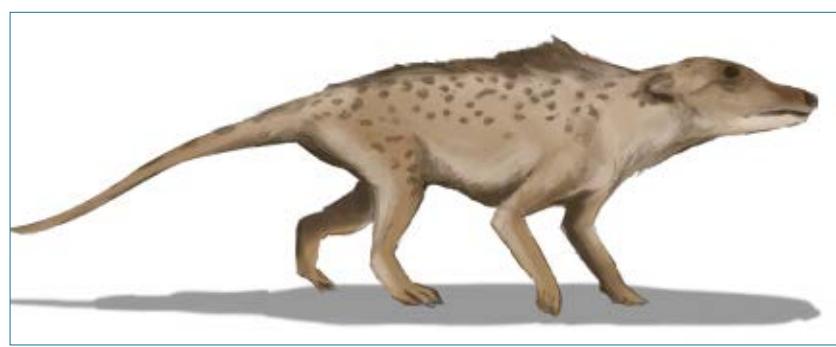
Finally, they gloss over the fact that there is a large morphological gap between *Dorudon* and living whales (the odontocetes and mysticetes). Some published information also includes *Basilosaurus*, which is a bit of a red herring! It was a creature which lived in shallow seas and resembles a giant eel but is not considered to be an ancestor of modern whales. Barbara Jaffe Stahl, a vertebrate paleontologist and evolutionist, pointed out that “The serpentine form of the body and the peculiar shape of the cheek teeth make it plain that these archaeocetes [like *Basilosaurus*] could not possibly have been the ancestor of modern whales.”<sup>14</sup>

### The astragalus

One thing which is shared by some of these four-legged fossil creatures is the shape of one of the ankle bones (the astragalus), which is similar to that of even-toed ungulates (artiodactyla). (Note that *Pakicetus* had five toes on the front legs and four toes on the back legs.) The ankle bones of *Pakicetus*, *Indohyus*, and living artiodactyls (like the deer, pig, and hippo) have a ‘double pulley’ astragalus, as shown in figure 4.



**Figure 4.** Various astragali from Thewissen et al.<sup>3</sup>



**Figure 5.** *Pakicetus*, a wolf-like creature once claimed to be an amphibious intermediate showing the transition from land to sea, but now known to have been fully terrestrial.

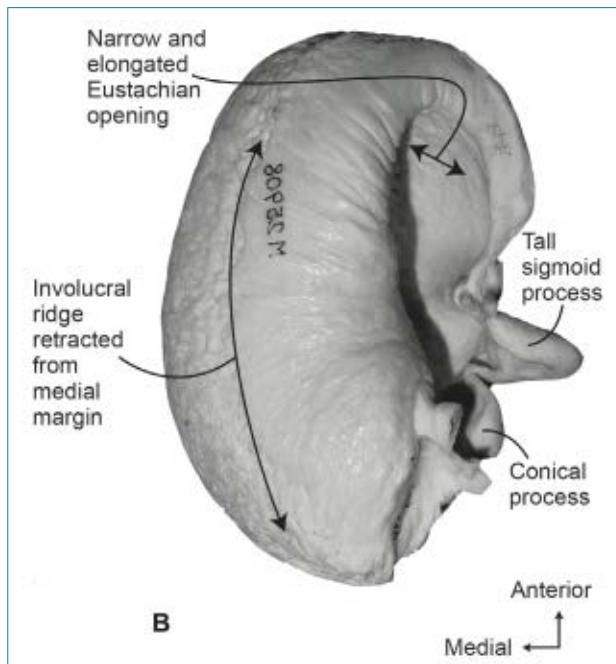
The existence of the double-pulley astragalus in the fossil archaeocetes is one of the reasons that evolutionists consider whales to be related to artiodactyls. However, this conclusion is driven by a prior commitment to common descent. An alternative hypothesis is that this is an example of shared design consistent with a terrestrial lifestyle.

### Archeocetes

The archaeocetes are all claimed to be extinct ‘whales’ and include the following families: Pakicetidae, Ambulocetidae, Remingtonocetidae, Protocetidae, and Basilosauridae (which includes *Dorudon*). Evolutionists often refer to pakicetids and ambulocetids as ‘walking whales’.

### Pakicetidae

The best-known pakicetid is *Pakicetus inachus* (figure 5), which evolutionists believe to be related to the ancestor of whales. It is now known to have been a dog-sized carnivorous quadruped with hooves, living on land.<sup>3</sup> It was found in



**Figure 6.** Tympanic bulla of *Balaenoptera borealis* (figure 16 from Ekdale et al.<sup>16</sup>)

Pakistan in lower Eocene rocks that are claimed to be about 50 Ma.

The claim that it is related to the ancestor of whales is based on the thick, bony wall (involutrum) of the middle ear (the auditory bulla) and the relatively heavy, anvil-shaped small bone in the middle ear (incus), which are the only things linking *Pakicetus* to living cetaceans. The thick wall of the involutrum is thought to be an adaptation to underwater hearing, along with other unique features of the ear of extant whales. Yet almost everyone agrees that *Pakicetus* lived on land. The question is, why did an animal have ears which were ‘adapted to underwater hearing’ when it was a land creature?

Another claim that is still current is that the auditory bulla had a sigmoid process, like that of living whales. However, the feature that was identified as the sigmoid process in *Pakicetus* is in fact a flat, plate-like ridge.<sup>15</sup> The sigmoid process of living whales and dolphins (figure 6) is finger-like and S-shaped (hence sigmoid).

Comparison of these tympanic bullae shows that *Pakicetus* did not have a sigmoid process. So the idea that *Pakicetus* was a walking whale is based mostly on the fact that it had an involutrum and robust ear bones. Evolutionists will protest at this and say that *Pakicetus* also had other characteristics in common with other archaeocetes, like, for example, *Ambulocetus* and *Dorudon*. This claim is based on the assumption that these were ancient whales which

is questionable since none of these creatures was very whale-like.

### Ambulocetidae

There is only one known species of Ambulocetid and that is *Ambulocetus natans*.<sup>17,18</sup> It was found in Pakistan in rocks which evolutionists think are roughly 48 or 47 Ma old. It is almost always shown in a swimming posture, which is odd given that its name means swimming (*natans*) walking (*ambulo*) whale (*cetus*). There is no reason to doubt that it could walk as shown in figure 7.

The fact that it had a double-pulley astragalus like antelopes and hippos is consistent with an ability to walk on land. Nevertheless, it seems likely that *Ambulocetus* was amphibious and could probably have moved through water much like an otter, using its powerful hind legs to propel itself.

### Protocetidae

This family includes creatures like *Maiacetus*, *Niparajacetus*, and *Peregocetus*, which are all very similar to each other and to *Ambulocetus*.

*Maiacetus* was discovered in 2000, and additional material was found in 2004.<sup>19</sup> These fossils were recovered from early middle-Eocene rocks in Pakistan, which evolutionists believe to be around 47 Ma old. One specimen is of an adult female and includes the skull and partial skeleton of a single large near-term foetus, which is positioned for a head-first delivery, typical of land mammals. Therefore, this creature must have been able to walk on land. This fact only goes to highlight the huge difference between the amphibious protocetids and *Dorudon*, which was an obligate aquatic animal.

### Dorudon

*Dorudon* (figure 8) was a fully marine creature with very small ‘hind legs’ of uncertain function which probably did not have a double-pulley astragalus.<sup>20</sup> The hind limbs may have functioned as claspers to enable copulation. It has been found in various locations and is claimed to have lived 40 to 34 Ma ago. Evolutionists point to similarities, mainly of the skull and teeth, as evidence that *Dorudon* evolved from creatures similar to *Ambulocetus*.

The shape of the bones at the end of the tail of *Dorudon* (wider than they are high) is consistent with the presence of a fluke. However, no-one has been able to describe the process for the change to propulsion through the water by a fluke. The fluke appears suddenly in the fossil record. There are no fossils showing the gradual appearance of a fluke.

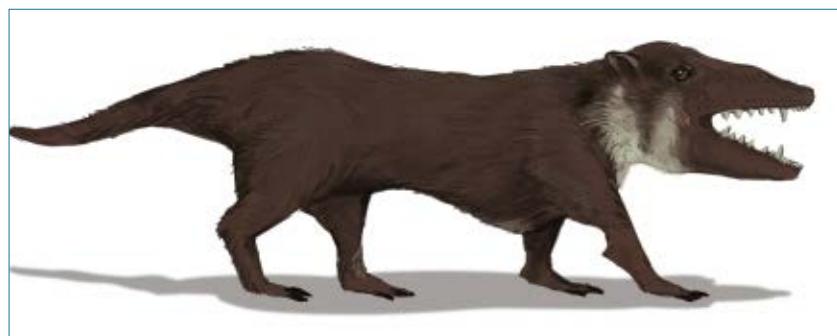
In fact, it is difficult to see how this transition could occur gradually as the creatures would have been unlikely to survive the reduction in the size of the hind limb while the fluke was still developing. Protocetids probably relied on their large, powerful hind legs to propel themselves through the water. It seems likely that the process of natural selection would have caused any possible intermediate with smaller legs to become extinct, since it would have been unable to move as efficiently as its ancestors. There are other problems, since this change would have had to come about at the same time as the creature adapted to a fully marine lifestyle, with the ability to cope with the salt from the sea, underwater hearing, giving birth and suckling underwater, to name but a few of the features required for life in the sea.

All these things illustrate the huge difference between *Pakicetus* and *Dorudon*, yet evolutionists believe that the change could have occurred in less than 10 Ma. This seems hardly credible when compared with the belief that humans and apes evolved from a common ancestor in about 5 Ma. There is not enough time for all the new features required to change the hypothetical common ancestor of *Pakicetus* and *Dorudon* into a creature like *Dorudon*, which appears well designed for life in the sea, especially when one considers that the supposed evolution of humans did not require any completely new features.

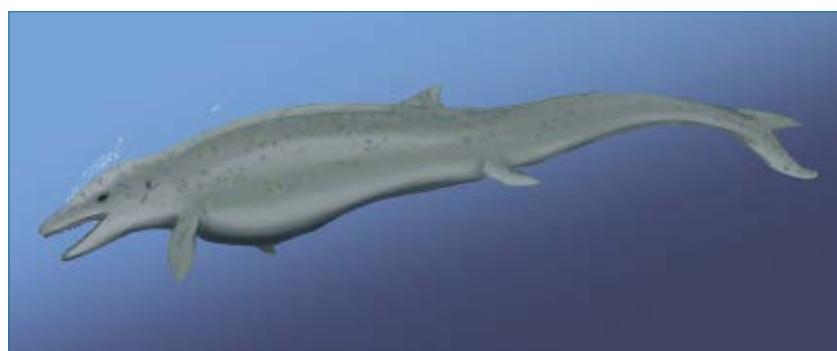
Not only is there a huge gap between the protocetids and *Dorudon*, there is also an enormous gap between a creature like *Dorudon* (shown above) and a modern cetacean like the dolphin (figure 9).

The shape of the head of *Dorudon* was unlike living cetaceans. *Dorudon* had a long, narrow snout. Its teeth were heterodont (teeth of different sizes and shapes) and included incisors, canines, premolars, and molars. The largest cheek teeth of *Dorudon* were triangular, blade-like, had two widely separated roots, and had serrated crowns. Living odontocetes have teeth with a single root and typically have only a single cusp. Their teeth are all a similar shape (homodont).

The so-called walking whales had nostrils which, even though they were in some cases set back on the snout, are clearly nostrils and have no resemblance to a blowhole. It should be noted that a blowhole involves more than simply moving the nostrils to the top of the head. There is a



**Figure 7.** A reconstruction of *Ambulocetus*, showing how it could have walked.



**Figure 8.** *Dorudon* was a fully marine creature, claimed to be an evolutionary ancestor of living whales.

complex network of nerve endings located in the region of the blowhole. These nerves end with pressure sensors, so the animal knows when its blowhole is clear of the water, and it is safe to breathe. Furthermore, the airways connecting the blowhole to the windpipe follow a different route from that in terrestrial mammals. The major difference is that the airways from the nostrils and the mouth do not connect, so a dolphin cannot breathe through its mouth.

Any evolutionary account must explain how these differences originated through the process of random mutation and natural selection in less than 10 Ma.

### Missing fossils

The fact that there are no fossils of the extant (modern) whales in rocks considered by creationist geologists to have been laid down during or shortly after the Flood has been suggested to be a problem for creation biologists. According to the traditional reading of Scripture, the archaeocetes and extant whales would have co-existed in the pre-Flood oceans and therefore should have been fossilized together. So the argument goes that the fact that extant whale fossils are never found with the archaeocetes shows that they must have evolved later. However, this argument is weak because there are many cases of creatures which are alive today yet are missing from large parts of the geological column.



**Figure 9.** Dolphin

## Discussion

Having reviewed the fossil evidence, it seems that the evolutionary origin of whales is not proven. The claim that the fossils reviewed above are an example of macroevolutionary change and the suggestion that the ancestors of whales walked off Noah's Ark can both be rejected. It is important to note that the evidence is focused primarily on the anatomical features of the skeletons of the supposed ancestors of extant whales. The proposed evolutionary transition might appear to be more plausible when only the skeleton is considered. However, this overlooks the biggest challenge, which is the origin of the integrated systems which enable life in the sea (this will be discussed in part two).

Nevertheless, the fossil 'archaeocetes' are presented as evidence of an evolutionary transition from fully terrestrial to fully marine creatures. It is believed that the ancestor of whales was some sort of artiodactyl (even-toed hooved animals, like pig, deer, and hippopotamus). Currently evolutionists consider that *Indohyus*, a semi-aquatic artiodactyl, is closely related to the ancestor of whales. However, it is important to emphasize that the evidence does not provide a series of credible transitional fossils. The only feature which links *Indohyus* to whales is the involucrum (the thickened bony wall of the middle ear), although some have even disputed the existence of the involucrum in *Indohyus*.<sup>21</sup> Nevertheless, there were other creatures (for example *Pakicetus*, *Ambulocetus*, and *Maiacetus*) which evolutionists claim are ancestors of whales because of the involucrum, which is believed to be an adaptation to underwater hearing.<sup>12</sup> Sharing this solitary feature with whales scarcely justifies the confidence of evolutionists that whales evolved from these walking animals. The evolutionary theory is further weakened by the fact that another semi-aquatic artiodactyl, the hippopotamus, does not have an involucrum; neither do beavers nor otters, which are semi-aquatic.

Another part of the evolutionary account is the fact that fossils like *Pakicetus*, *Ambulocetus*, and *Maiacetus* have ankle bones with a double-pulley astragalus (ankle bone). This is a feature shared with artiodactyls. Therefore, these extinct creatures are considered to be artiodactyls because of the double-pulley astragalus and whales because of the involucrum. Of course, living whales do not have ankles, so the only things that link them to the so-called archaeocetes are the thickened ear bones and the involucrum of the auditory bulla.

*Dorudon* is also considered to be closely related to an ancestor of whales. This creature lived in the sea and had very small hind limbs and possibly a double-pulley astragalus. This and other features of the skeleton and teeth are seen as evidence that creatures like *Pakicetus*, *Ambulocetus*, and *Maiacetus* were ancestors of *Dorudon*. However, there is a massive difference between *Dorudon* and living whales.

It is clear that an alternative interpretation is needed. There was a group of extinct creatures which were paddle swimmers; *Ambulocetus* is a good example. These creatures appear to have been amphibious and would also have been able to walk on land. However, *Pakicetus* is considered by many to have been fully terrestrial, although one expert on whale evolution (Philip Gingerich) considers this reconstruction to be erroneous because it is based on bones of a terrestrial creature that have been incorrectly referred to as *Pakicetus*.<sup>22</sup> According to Gingerich, *Pakicetus* was very similar to *Ambulocetus*. If *Pakicetus* was indeed more similar to these amphibious creatures, then its status as a morphological intermediate, linking land animals to the paddle-swimming creatures, is less obvious.

From the point of view of creation biology, there appear to have been three different kinds of extinct creatures which had an involucrum. Terrestrial creatures like *Indohyus*, which may have been amphibious, the amphibious paddle swimmers, like *Ambulocetus* (and also, according to Gingerich, *Pakicetus*) and fully marine creatures like *Dorudon*, which, like *Basilosaurus*, had very small hind limbs of uncertain function, thought by many to be reproductive claspers. The morphological differences between these groups are considerable, and the belief that they represent a series of transitional fossils is because of an *a priori* commitment to evolution. There is an especially large gap between extant whales and creatures like *Dorudon*.

A creation biologist would consider that the fossil evidence is consistent with the concept of distinct basic types

or created kinds, specifically designed for life in different environments. Some experts in the science of baraminology (the study of created kinds) have studied whale baraminology. There is evidence for at least five baramins: baleen whales, beaked whales, sperm whales, other toothed whales, and the archaeocetes.<sup>23</sup> A study of baleen whales suggests that there are at least three baramins of baleen whales.<sup>24</sup>

## Conclusion

Given the evidence reviewed here, the evolutionary account of the origin of modern whales appears to be unsupported. The fossils which are claimed to be closely related to the ancestors of whales belong to three distinct groups of extinct animals defined as follows:

- terrestrial creatures with an involucrum (e.g. *Indohyus* and *Pakicetus*)
- amphibious paddle swimmers with an involucrum and double-pulley astragalus (e.g. *Ambulocetus*, *Maiacetus*, and similar creatures)
- toothed marine creatures with small hind limbs that possibly functioned as claspers (e.g. *Dorudon*, and *Basilosaurus*).

Each of these extinct groups appears to have had a unique set of features and was designed for a specific lifestyle; terrestrial, amphibious, or marine.

Today there are at least three ‘families’ of extant whales; the mysticetes (baleen whales) and two families of odontocetes (toothed whales and dolphins). Future research could be directed to further defining the various basic types or baramins of extant whales and the so called archaeocetes.

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# Amyloids having sequence-, regio-, and stereo-selective properties don't form under plausible prebiotic conditions

Royal Truman

It has been claimed that a synthetic amyloid can direct the sequence-, regio-, and stereo-selective condensation of amino acid synthesis, thus allegedly supporting the Amyloid world hypothesis. Substrate peptides constructed from alternating arginine and phenylalanine residues were mixed with a templating octapeptide one to three residues longer, consisting of alternating phenylalanine and aspartic acid. However, the three amino acids (aa) are not believed to have existed in measurable quantities prebiotically. Preferences were found towards some single aa addition to a substrate one residue shorter than the template. Contra these results, when the substrate was two residues shorter aa addition was preferred in the absence of a template in four out of five aa tested. When the substrate was three residues shorter two combinations of three aa added were preferentially L-enantiomers, but in only ~1% yields. However, the statistically most likely mixtures produced by chance would have had very little or no template present. In this case, addition of D-enantiomers was always favoured with no significant preference for various aa. The regio-selectivity experiments were conducted by mixing long linear substrates and templates synthesized with no side-chain reactions, which would have been unavoidable had they been produced incrementally under natural conditions. All the effects would only be limited to exceedingly exotic laboratory designs, negligibly affecting at most three aa in an entire arbitrarily long polypeptide. The template had to be chemically modified at both termini, the substrate at the C termini, and the N end activated with CDI. Ideal stoichiometries were used in implausibly high, pure concentrations. Mixing and formation of amyloids required agitation at 800 rpm at 37°C for ~18 hours.

The Amyloid world theory for abiogenesis has been gaining popularity at the expense of the RNA world theory.<sup>1</sup> Many allegedly life-relevant properties have been attributed to synthetically produced amyloids. In a 2018 review article, Maury wrote:

“Rout *et al.* [2] showed that an amyloid can direct the sequence-, regio-, and stereo-selective condensation of amino acid synthesis.”<sup>3</sup>

These are three topics widely discussed in origin of life (OoL) circles. Correct *sequences* are necessary to form suitable peptides. *Regiospecificity* is necessary or nucleotides and amino acids (aa) would undergo the wrong chemical reactions. And *stereoselectivity* is a major problem since the key biochemicals to support life require that specific stereoisomers only be used.

The significance attributed to this paper is that allegedly,

“... it demonstrates that an amyloid formed from short peptides can direct the synthesis of its own constituent peptides under plausible prebiotic Earth conditions.”<sup>2</sup>

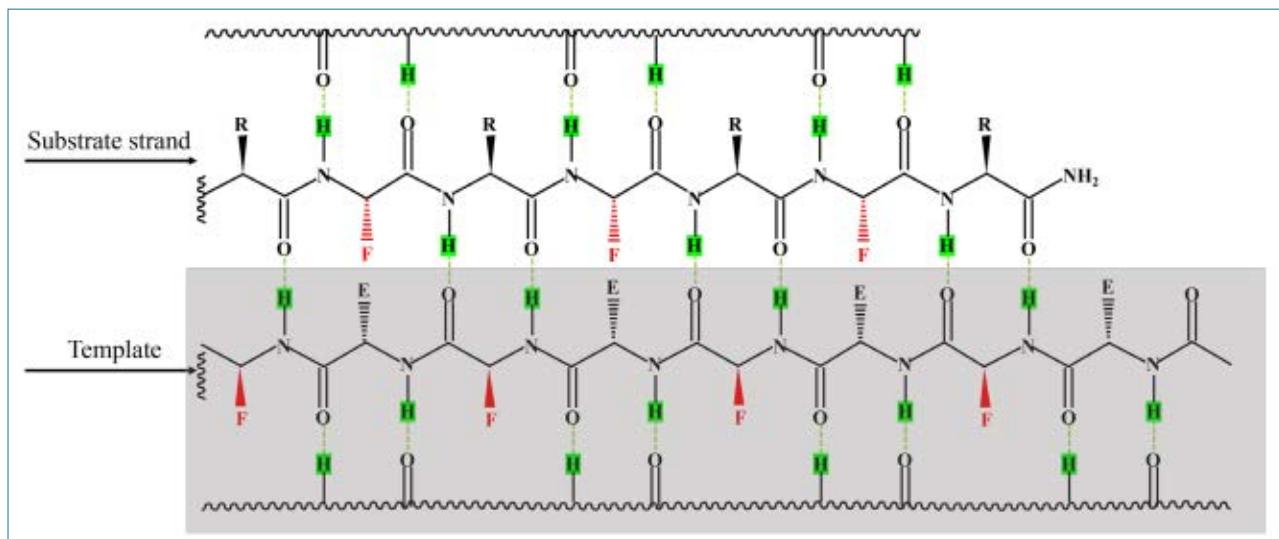
Examination of the paper revealed that this is not supported by the experiments reported. The constituent amino acids and peptides were already provided in pure,

concentrated, and activated forms. We decided to examine the other claims attributed to this publication.

## Biological proteins and amyloids

Cells manufacture proteins and amyloids having the three important properties mentioned above, thanks to the genetic code and pre-existing homochiral enzymes. It is also well known in molecular biology that special secondary structures in proteins, such as  $\alpha$ -helices and  $\beta$ -sheets, only work for a restricted variety of aa residues at each position. The structures must not include side-chain reaction products, and only L-aa must be used.<sup>4</sup> The secondary structures benefit from many H-bonds and an arrangement where hydrophilic side changes are oriented towards stabilizing interactions with water and the hydrophobic side chains are buried away from water.

Figure 1 shows part of a  $\beta$ -sheet, illustrating the large number of stabilizing H-bonds (shown in green). Only three types of aa were used, as in the experiments by Rout *et al.*, with the most used phenylalanine (F) shown in red.<sup>2</sup> Stable  $\beta$ -sheets are a prerequisite to form the amyloid fibrils they reported.



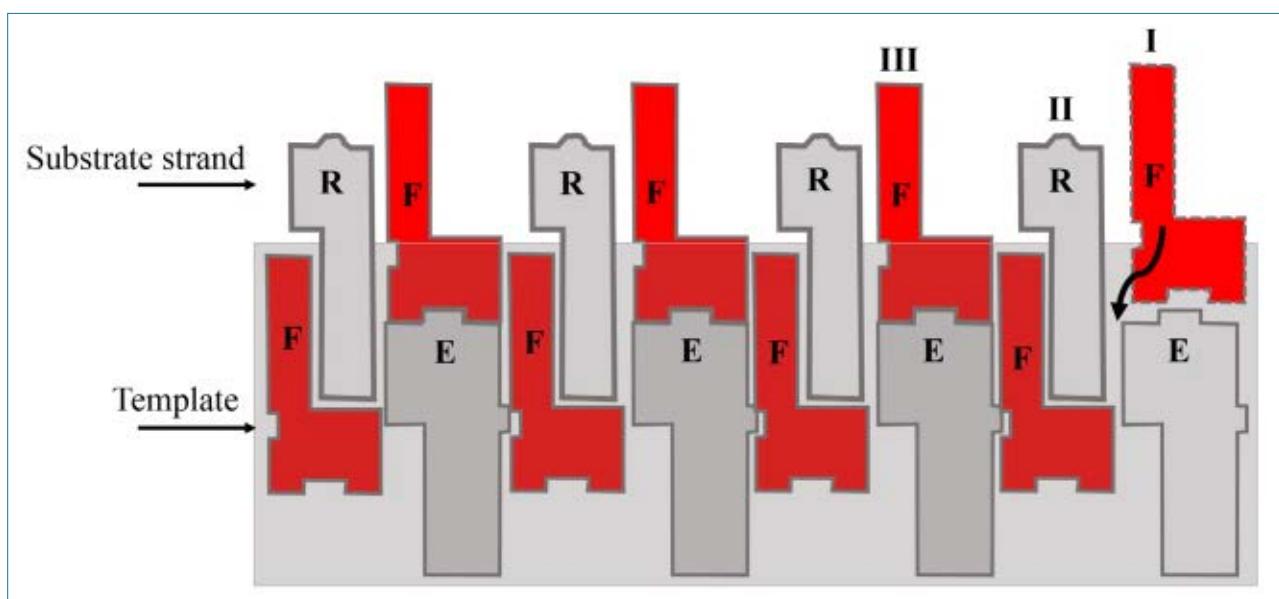
**Figure 1.** Antiparallel  $\beta$ -sheet using substrate and template sequences examined by Rout *et al.*<sup>2</sup> H-bonds are shown by the green H atoms they involve. R = arginine, F = phenylalanine, E = aspartic acid. Template peptide shown in grey box. Rout *et al.* did not describe the  $\beta$ -sheets produced in their experiments; this is our suggestion.

Decades of research have provided a set of rules and techniques chemists can use to synthesize these peptide secondary structures. Typically, aa from a biological source are isolated, and the end carboxyl and/or amino protons are activated by substituents, enabling them to react in water, or more often, in an anhydrous solvent. The question of interest here is whether various reported laboratory experiments reflect plausible prebiotic conditions.

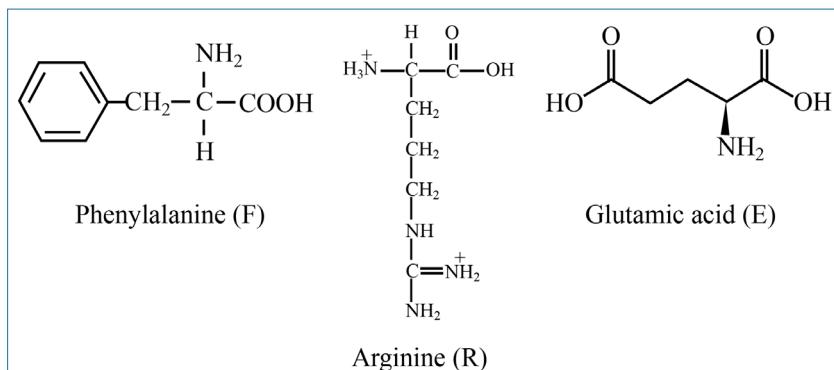
#### Amyloids from simple synthesized $\beta$ -sheets

The manner in which existing  $\beta$ -sheets constrain which residue is added can be illustrated by a puzzle, whereby correctly placed pieces determine which piece would fit in a new position. Figure 2 illustrates the strategy apparently used by Rout *et al.*

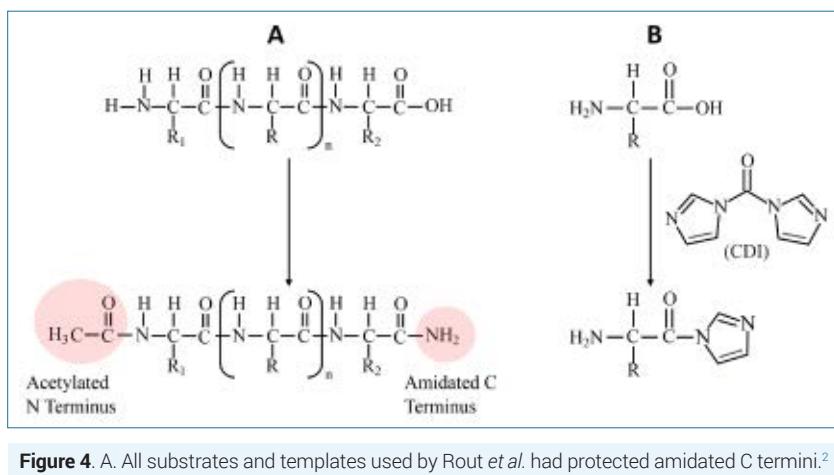
Addition of aa with suitable properties to extend an existing  $\beta$ -sheet would be favoured, since this results in



**Figure 2.** Existing  $\beta$ -sheets, like an incomplete puzzle, provide guidance for amino acid selection. Here the puzzle sizes and shapes represent steric constraints and electrostatic influences of individual amino acids. R = arginine, F = phenylalanine, E = aspartic acid. In position I, addition of the amino acid F would be favoured.



**Figure 3.** Chemical structure of phenylalanine (F), arginine (R), and glutamic acid (E), used to form peptide substrates and templates by Rout *et al.*<sup>2</sup>



**Figure 4.** A. All substrates and templates used by Rout *et al.* had protected amidated C termini.<sup>2</sup> In addition, the templates had a protective acetylated N-terminus to protect from degradation. Activated amino acids can only add to the still free N-terminus of the substrates. B. All amino acids were activated with CDI (1,1'-carbonyldiimidazole).

a thermodynamically lower free-energy state. Suitable properties include having the correct chirality, steric interactions, and hydrophobic or hydrophilic nature to complement the counterpart residues. The principle can be visualized using figure 2, where a specific puzzle piece (aa F) would fit well at position I.

### Substrates and templates mixed to form amyloid substances

Rout *et al.* designed peptide substrates and templates having an alternating hydrophilic and hydrophobic L-aa residue in order to produce amphipathic  $\beta$ -strands.<sup>2</sup> The peptides to which activated aa could add were called *substrates*. In almost all the experiments, the peptides consisted of the aa R = arginine and F = phenylalanine. The amino end of the substrates contained a free  $-\text{NH}_2$  group able to react with an activated aa carboxyl group.

*Template peptides* almost always had the structure  $(\text{FE})_4$ , where F = phenylalanine, and E = glutamic acid. These were

called template peptides, since they organized the substrates into  $\beta$ -sheets. These were designed so that the R and F groups would be chemically complementary in order to produce amyloid-like substances.

Both substrate and template peptides were modified chemically before being used, as mentioned in the section “Experimental details” below, and shown in table 1. This already eliminated any claim to plausibility for OoL purposes.

The three aa used to create these peptides were chosen so that both the template and substrate would be soluble at neutral pH and would also form an amyloid when mixed in high concentration. Their chemical structure is shown in figure 3.

### Experimental details

The substrates and template were modified chemically, as shown in figure 4A. In addition, all aa were first activated with the condensing agent CDI (1,1'-carbonyldiimidazole,  $(\text{C}_3\text{H}_3\text{N}_2)_2\text{CO}$ ). This process alone also eliminated any claim to plausibility for OoL purposes (see below).

The experiments based on four template/substrate pairs will be summarized next. The template and substrates used in the first three experiments are shown in table 1, aligned to show the longer template ‘overhang’, which helped select aa which added to the substrate.

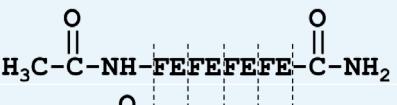
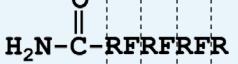
#### Experiment 1

In the  $\text{R}(\text{FR})_3/(\text{FE})_4$  substrate/template experiment, the template contained one more residue than the substrate. An insoluble aggregate (fibril) was produced.

Five activated aa (phenylalanine (F), aspartic acid (D), glycine (G), valine (V), and arginine (R)) were added individually, first to  $\text{R}(\text{FR})_3$  alone and then to the  $\text{R}(\text{FR})_3/(\text{FE})_4$  amyloid. The yields of single aa addition are shown in table 2.

In spite of having used activated aa in high concentrations with rapid stirring, the single addition yields for these amyloids ranged from 3.5% to 50%, with the highest for phenylalanine, the optimal aa to extend the  $\beta$ -sheet. The key observations are:

**Table 1.** Template and substrates mixture to form amyloids. The substrates are shown in a reversed orientation to form antiparallel β-sheets.

Experiment	Peptide	Abbreviation	Structure
	Template	(FE)4	
Experiment 1	Substrate	R(FR)3	
Experiment 2	Substrate	(FR)3	
Experiment 3	Substrate	R(FR)2	

**Table 2.** Yields of activated single amino acid addition to substrate R(FR)<sub>3</sub> alone, and to R(FR)<sub>3</sub>/(FE)<sub>4</sub> amyloid. Room temperature, 18 h reaction times. F = phenylalanine, D = aspartic acid, G = glycine, V = valine, and R = arginine. From Supplementary Tables 1 and 2 of Rout et al.<sup>2</sup>

Amino acid <sup>a)</sup>	Conditions <sup>b), c)</sup>	% yield	Ratio (L/D) <sup>d)</sup>
F	R(FR)3	2.8	0.6
	R(FR)3/(FE)4 amyloid	50	3.9
V	R(FR)3	3.2	0.98
	R(FR)3/(FE)4 amyloid	48	6.2
D	R(FR)3	33	—
	R(FR)3/(FE)4 amyloid	35	—
R	R(FR)3	2.6	—
	R(FR)3/(FE)4 amyloid	3.5	—
G	R(FR)3	13	—
	R(FR)3/(FE)4 amyloid	30	—
L	R(FR)3	—	0.9
	R(FR)3/(FE)4 amyloid	—	3.1
Y	R(FR)3	—	0.7
	R(FR)3/(FE)4 amyloid	—	2.0
W	R(FR)3	—	1.0
	R(FR)3/(FE)4 amyloid	—	3.2

a) Amino acid: 100 μM L-amino acids used for the % yield experiments, DL-amino acids for the ratio (L/D) experiments

b) R(FR)<sub>3</sub> substrate alone: 100 μM

c) R(FR)<sub>3</sub>/(FE)<sub>4</sub> amyloid formed using 100 μM R(FR)<sub>3</sub> with 130 μM (FE)<sub>4</sub>

d) Lower L/D was obtained when amino acid concentration < 100 μM.

- The reaction of five activated aa added with very different preferences to the arginine (R) end of the amyloid. Only a single residue was added.
- In this experimental setup, the amyloid was stereoselective for the L-enantiomer.
- When using the substrate alone, more D-enantiomers were selected—the opposite of what life needs!

#### Experiment 2

In the (FR)<sub>3</sub>/(FE)<sub>4</sub> substrate/template experiment, the template contained two more residues than its partner. An insoluble aggregate (amyloid) was produced.

The activated aa F, D, G, V, and R were added to (FR)<sub>3</sub> alone and then to the (FR)<sub>3</sub>/(FE)<sub>4</sub> amyloid in stoichiometric proportions. Now the amyloid no longer favoured single addition of the hydrophobic phenylalanine and valine, *contra* the results from experiment 1, shown in table 2. This is not surprising, since the aa added now aligned with a different position with respect to the template, see figure 2, position II. Instead, the yield of the now shorter amyloid was higher vs. for substrate (FR)<sub>3</sub> but *only for arginine*. Remarkably, for the four other aa the single addition yield was *now much higher when using only the substrate*.

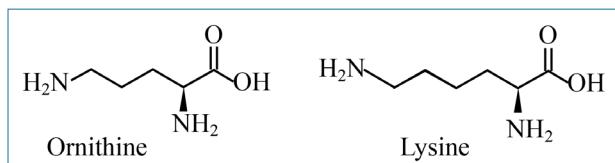
Unfortunately, preferences for L- vs D-enantiomer (stereoselectivity) were not reported. We expect the substrate acting alone to favour addition of the D-enantiomers as before.

The key observation is:

- In the presence of the same template, substrates having different lengths produce contradictory yield patterns of single addition of the aa.

#### Experiment 3

In the R(FR)<sub>2</sub>/(FE)<sub>4</sub> substrate/template experiment, the intention was to test whether a short substrate could provide three end-residue templating aa addition positions. However, the R(FR)<sub>2</sub> + (FE)<sub>4</sub> mixture remained soluble and did not form an amyloid.

**Figure 5.** Chemical structure of ornithine and lysine

Since experiment 2 (using  $(FR)_3/(FE)_4$ ) did form an amyloid, if the end R group in the  $R(FR)_2 + (FE)_4$  new mixture would react with a phenylalanine, an amyloid could be produced. Therefore, the researchers added activated DL-phenylalanine and DL-arginine at the higher concentration of  $200 \mu\text{M}$  to the mixed  $R(FR)_2 + (FE)_4$ .

Low yields of addition products were obtained, as shown in figure 4 of reference 2, including single and double additions having a mixture of D- and L-enantiomers. Remarkably, of the triple additions, two were generated by far in the highest relative proportion, namely L- $(FR)_4$  and L-FF( $FR)_3$ , i.e. using only L-enantiomers. Apparently, the three end positions of the template had a small directing effect. However, taking the 2:1 molar stoichiometry into account indicated that each triple addition yield was only about 1% (estimated from figure 4 of reference 2).

Unfortunately, addition preferences for a variety of different aa were not reported.

The key observation is:

- A carefully crafted templating  $\beta$ -sheet was able to favour addition of three activated L-aa to a peptide containing a complementary  $\beta$ -sheet in a yield of about 1%.

#### Experiment 4

In a final experiment the substrate used was  $(OV)_4 = (OVOVOV-NH_2)$ , and the template was V( $DV)_4 = (AcVDVDVVDV-NH_2)$ . O refers to ornithine, whose structure is shown in figure 5.

It is not clear why the non-biological ornithine was selected for study instead of lysine, which differs by having one more  $\text{CH}_2$  on the side chain.

The  $(OV)_4$  molecule contained four side-chain -NH<sub>2</sub> groups and one N-terminal which could react with an aa to form an amide bond. Activated valine and activated phenylalanine each added to the N-terminal amino about a fifth of the time, whereas valine added to the amyloid N-terminal amino 65% and phenylalanine 85% of the time, i.e. the reaction was regioselective when using the amyloid.

The substrate  $(OV)_4$  underwent sizeable degradation after hydrolysis at  $90^\circ\text{C}$  for 6 h, whereas almost none was reported for the amyloid.

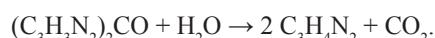
The key observations are:

- Large insoluble amyloid fibrils can sometimes hinder the functional groups on side chains from reacting.
- Large insoluble amyloid fibrils can be thermally stable.

#### Discussion

Carefully designed and executed laboratory experiments *per se* have little to say about prebiotic chemistry. In fact, none of the results above are surprising from a chemical point of view. The fundamental issues are: plausibility under non-planned putative prebiotic conditions, and the interpretation of the laboratory results. Can they be generalized in any useful manner or are they uniquely designed laboratory artifacts? Therefore, careful thought is necessary about the key details of the experiments.

1. None of the substrate and template peptides were used in their natural form. All had their C termini protected (amidated).
2. The template peptides also had a protective acetylated N-terminus to protect them from degradation. These two synthetic methods to protect peptides are well known to chemists.<sup>5</sup>
3. The end-carboxyl groups of all the free aa were activated with the condensing 1,1'-carbonyldiimidazole (CDI). CDI is readily destroyed in water by the following reaction:



This is a problem in general with condensing agents. By their very nature of removing water from a condensation polymerization, they are readily degraded in water itself. Therefore, standard practice is to conduct the reaction in an anhydrous solvent such as tetrahydrofuran, chloroform, benzene, or dimethylformamide, none of which would have been present as a solvent in a prebiotic earth.<sup>6</sup> The authors don't mention which solvent was used, only that two equivalents CDI per aa were used, *added on ice*.

4. To form amyloids, they purchased substrate peptides and template peptides which were extensively purified by reverse-phase HPLC and then dissolved in 50 mM sodium phosphate buffer, pH 7.4.
5. Next, 100  $\mu\text{M}$  substrate and 120–130  $\mu\text{M}$  template peptide were mixed in water and agitated in an Eppendorf thermomixer agitating at 800 rpm at  $37^\circ\text{C}$ . Formation of fibrils was monitored using circular dichroism spectroscopy and appeared to reach equilibrium within a few hours. (It would have been easy to do some experiments rotating at, for example, 1 or even 50 rpm and see if fibrils would be produced.)
6. Since this formed flocculent aggregates, they were “sonicated (10 s, 20% power, Bandelin Sonoplus HD 2070 with MS73 microtip) to improve liquid handling before performing the addition reactions.”<sup>2</sup>

#### Prebiotically absurd conditions

Although we are focusing on a specific influential paper, many recurring principles characteristic of the OoL literature will be identified. Those not familiar with OoL publications might be mystified as to what the present experiments

could possibly have to do with putative prebiotic chemistry. Reviewing the paper by Rout *et al.* shows it to be replete with phrases like *prebiotic conditions*, *prebiotic reaction*, *prebiotic setting*, *prebiotic composition*, and *prebiotic system*.<sup>2</sup>

What aspect of these experiments might have been meant to be representative of prebiotic conditions? One could evaluate every laboratory parameter used which were indispensable to obtain the reported results:

- Use of L-only peptide substrates and templates in extraordinarily high concentrations and ideal stoichiometry.
- Perfectly alternating hydrophilic and hydrophobic amino-acid residues known to form amphipathic  $\beta$ -strands.
- Perfectly complementary sequences for the substrates and templates.
- Elaborate measures to purify the substrates and templates before combining them.
- Capping of the amino and carboxyl end groups of all the templates.
- Capping of the carboxyl end groups of all the substrates.
- Activation of all aa using CDI that would hydrolyze quickly.
- Agitation in special equipment at 800 rpm at 37°C for at least 18 hours.
- Use of a closed container to force the components to interact.
- Termination of the experiments after the highest yields have been attained.
- Use of sodium phosphate buffer solution to ensure a pH of 7.4.
- Sonication to improve liquid handling.

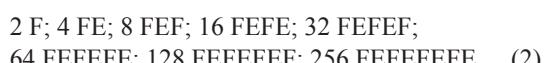
Perhaps at least the three aa used to create the substrates and templates (phenylalanine, arginine, and glutamic acid) were the major aa expected to be found prebiotically? The 2023 publication by Kobayashi *et al.* was consulted, arguably the most careful simulation of aa produced from all sources under the most realistic reducing atmosphere.<sup>7</sup> Absolutely none of these three aa were obtained. As a second test, the best review of all substances extracted from the Murchison meteorites is probably the 2017 review paper by Koga *et al.*<sup>8</sup> Of the three aa only trace amounts of DL-glutamic acid were found.

Perhaps the peptides were based on realistic L-vs-D enantiomer ratios? If R(FR)<sub>3</sub> from experiment 1 had formed naturally it would have been part of a grand mixture of many DL-substances, such as:



since each aa could have a D- or L-enantiomer at each position.

These would have been mixed with all the enantiomeric template (FE)<sub>4</sub> alternatives and their precursor DL-enantiomers:



The researchers combined only pure L-RFRFRFR with pure L-FEFEEFEE, although all the alternatives would also have been present. Astonishingly, the individual L-peptides were prepared and co-located in a vast number of copies:

$$100 \mu\text{M R(FR)}_3 = 10^{-4} \times 6 \times 10^{23} = 6 \times 10^{19} \quad (3)$$

and

$$130 \mu\text{M (FE)}_4 = 10^{-4} \times 6 \times 10^{23} = 8 \times 10^{19} \quad (4)$$

each per litre.

Clearly, these experiments cannot be used to claim that amyloid fibrils were produced under plausible prebiotic conditions and that these led to sequence-, regio-, and stereo-selective addition of amino acids.

Casual readers are seriously misled.

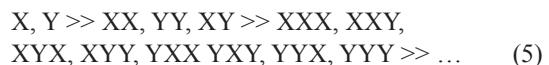
It is unfortunate that so many read OoL papers like these and simply quote the claims stated, blindly believing that the results would indeed have occurred with no intelligent guidance. A second universal practice in this genre of literature is to also publish quantitative values which were obtained after years of expert design and optimization. These two are then combined and widely distributed using wording such as, “*was obtained in high yields under plausible prebiotic conditions.*”

Of course, nobody objects to scientists entertaining themselves by exploring unusual artifacts in a laboratory. Since it is fundamental to a chemist’s training to optimize yields of a desired effect, many of us would have gladly collaborated with researchers like Rout *et al.* to find the best conditions possible. After all, one needs quantitative results to begin exploring the effect of changing parameter settings to realistic values.

## Conclusions

Let us perform a *Gedankenexperiment* and accept the trends reported in the above experiments. After all, a variety of other substrate and template peptides might someday also be examined.

Irrespective of the aa involved, condensation reactions in water are highly endothermic, so for any aa X and Y the aqueous concentrations of a substrate would be dominated by the smaller peptides:



The same applies for a template candidate.

Now, the proportion of a suitable substrate being co-located with a suitable template, having the requisite residue sequence and length (‘overhang’), would be many orders of magnitude lower than of the substrate alone. The data in table 2 shows that D-aa are preferentially added to substrates alone, whereas L-aa are preferentially added to

the amyloids. Since the former would be in vastly greater proportion long before any amyloids could form, the net outcome would be peptides preferentially having the wrong chirality. Therefore, the L-only peptides needed to produce amyloids could not form.

**Conclusion on stereo-selectivity:** The authors should have reported that if their experiments reflected prebiotic conditions, then far more peptides of the wrong chirality would have formed in the presence of amyloids.

In experiment 2, the yields of a single addition of activated F, D, G, or V were higher for the substrate than for the amyloid. Since far more substrate would have existed independent of co-located template, also for all the precursor peptides, this would be the dominant outcome. For the amyloid, the preference was dominant only for the aa R.

The opposite trends were reported for experiment 1, based on a substrate one aa shorter. As shown in table 2, the yield of the addition of R was about the same for the substrate and the amyloid. However, for the remaining F, D, G, and V, higher yields of addition occurred when the substrate was part of an amyloid. Consequently, mixtures of different substrates and templates would tend to cancel each other's effects.

Note that preferential addition of one aa was demonstrated for only five carefully selected aa of the 20 biological aa. The selectivity involved the addition of a single aa; was only possible thanks to the preceding chemical modifications of the substrate and template; required chemical activation of the aa; and resulted in considerable mutual cancelling of trends. Since substrate and template concentrations would not have been present concurrently in concentrations anywhere near  $10^{16}$  peptides/ml, this selectivity artifact would have been much too small to detect among a mixture of all condensation reactions occurring throughout nature. Virtually all would have involved very short peptides which would not form secondary structures.

The two L-only triple additions found in experiment 3 were only possible because an L-only substrate and template had been used. The precursor peptides would have already racemized, since kinetic and thermodynamic calculations show that the rate of racemization of pure L-peptide is faster than their rate of elongation in water under realistic conditions.<sup>9</sup>

In all these experiments one must not overlook that the stability of the amyloid fibrils was achieved only *after* huge, dense, insoluble materials had formed. This, in turn, was possible only thanks to the very high concentration of co-locate substrates and templates under rapid stirring. Any small precursors to the  $\beta$ -sheet would have been exposed to destructive hydrolysis over long geological times.

**Conclusion on sequence-selectivity:** Plausible prebiotic amyloids can provide neither measurable nor reliable sequence selectivity.

In experiment 4, valine and phenylalanine were found to add preferentially to the end amino group of the amyloid. Note that this required first forming an amyloid fibril under

extremely high concentrations using the substrate (OV)<sup>4</sup> and the template V(DV)<sup>4</sup>. The authors did not explain how the four ornithine molecules (O) managed to form about  $10^{16}$ /ml pure linear peptides, nor where all the pure templates with both ends chemically blocked could have come from.

During the substrate and template build-up process, several activated ornithine molecules would have added to the side chains, not being yet embedded in hindering amyloid. (This assumes both ends of the template had not been chemically blocked. Otherwise, the activated ornithine would only add to the side chains of the substrate). Each ornithine added to the side chain would now offer *two new competing -NH<sub>2</sub> groups*. Each elongation in the linear direction would only replace the amino group just 'consumed', while providing ever more opportunities for side-chain reactions.

**Conclusion on regio-selectivity:** Plausible prebiotic amyloids containing aa with side chains would not have formed, since this would have required a concentrated pool of only linear peptides *ab initio*.

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# Prebiotically plausible peptides don't self-assemble to produce useful catalytic amyloids

Royal Truman and Chris Basel

Plausibility for the Amyloid World Hypothesis has been claimed through experiments using synthetic zinc-binding heptapeptides able to hydrolyse p-nitrophenyl acetate. These were designed to form extended homochiral  $\beta$ -sheets. However, these peptides were tailor-made, based on known protein motifs, using histidine and other amino acids not expected to be prebiotically relevant, with impossibly high peptide concentrations. Replacing just one of the histidine residues eliminated almost all catalytic power. The indispensable  $Zn^{2+}$  cofactor concentration was a million times higher than that present in oceans and would have placed an upper limit on the maximum concentration of zinc-bound peptides. A build-up of amyloid fibrils could therefore not have occurred. Homochirality and side-chain protection were ensured through manual synthesis using the Fmoc high-temperature solid-state protocol. All peptides were also artificially protected by acetyl and carboxamide end-capping groups, eliminating any possibility of relevance to a prebiotic environment. The experiments suggest that fibrils capable of indiscriminate hydrolysis would have helped destroy the very polymers the amyloid world needs to have produced.

**M**aury, a leading advocate of the Amyloid World Hypothesis, claimed in a recent review article that amyloids synthesized under allegedly plausible prebiotic conditions exhibit a range of catalytic properties resembling biological enzymes.<sup>1</sup> The examples included aldolases;<sup>2,3</sup> ATPase;<sup>4</sup> carbonic anhydrase activities;<sup>5</sup> copper-mediated oxygen activation;<sup>6</sup> and ester hydrolysis.<sup>7</sup>

These studies had been expertly designed and executed by skilful chemists, using peptides that could not possibly have arisen pure and in high concentration under plausible prebiotic conditions. Multiple experimental details had been optimized to deliberately produce the outcome intended.

In the example of ester hydrolysis, Maury wrote:

“Rufo *et al.* showed that small, 7-residue amyloid-forming peptides form efficient catalysts of ester hydrolysis.”<sup>1</sup>

This is a broad statement, which seems to justify an examination of the experiments performed by Rufo *et al.*<sup>7</sup> in detail. We will focus on these experiments in this article.

## Catalytic hydrolysis using synthetic amyloids

Many enzymes hydrolyze amides, esters, or lipids, when necessary, in cells. An important class of enzymes binds a cofactor  $Zn^{2+}$  using three histidine (His, H) residues: two on a  $\beta$ -sheet separated by one residue and a third His from a neighbouring strand. The  $Zn^{2+}$  ion is known to help hold proteins in a folded state and to accelerate the rate of hydrolysis.

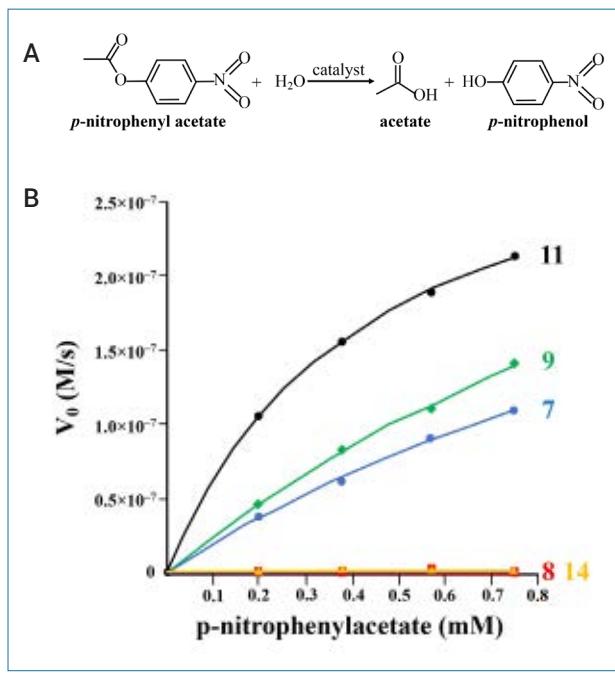
The researchers decided to synthesize 14 heptapeptides with alternating hydrophobic residues, designed to produce an amphiphilic  $\beta$ -strand and also bind  $Zn^{2+}$ . These  $\beta$ -strands could then associate in parallel layers via hydrophobic interactions to form large amyloids and catalyze the hydrolysis of various biochemicals, mimicking hydrolytic enzymes.<sup>8–11</sup>

Enzymes are often compared by determining their effectiveness to hydrolyse p-nitrophenyl acetate (pNPA) over a range of concentrations in the presence of a fixed concentration of enzyme, as shown in figure 1. During these kinetic experiments, Rufo *et al.* used peptide concentrations of 24  $\mu M$  mixed with 1 mM  $Zn^{2+}$  at a pH of 8. The analysis by circular dichroism (CD) spectroscopy to determine the presence of  $\beta$ -sheets used 0.5 mM  $Zn^{2+}$ .

The 14 heptapeptides examined are shown in table 1 and the chemical structures of the amino acids used by Rufo *et al.* in figure 2. Residues at peptide positions 2, 4, and 6 were selected which would bind  $Zn^{2+}$ .

## Results from the experiments

Isoleucine (Ileu, I) and Valine (Val, V) have greater, and Alanine (Ala, A) lower, propensity to form  $\beta$ -sheets than Leucine (Leu, L) does.<sup>12,13</sup> The peptides with stronger  $\beta$ -sheets (9 and 10 in table 1) were a little more active than 7, whereas 8, with lower  $\beta$ -sheet propensity, was inactive, as mentioned in table 1. Catalytic activities were determined based on Michaelis–Menten kinetics.<sup>14</sup>



**Figure 1.** Hydrolysis of p-nitrophenyl acetate to measure catalytic effectiveness, using 25  $\mu\text{M}$  peptide catalyst mixed with 1 mM  $\text{ZnCl}_2$  at pH 8. A. The hydrolysis reaction is shown. B. Curve fit to the Michaelis–Menten equation. Peptide 11 has not reached its constant maximum ( $V_{\max}$ ) value yet. The amyloid catalysts are defined in table 1. (B was redrawn after Rufo *et al.*<sup>7</sup>)

Careful design and experimentation led to peptide 11 having the best catalytic effects:  $k_{\text{cat}}/K_M = 62 \text{ M}^{-1} \text{ s}^{-1}$  and  $k_{\text{cat}} = 2.60 \times 10^{-2} \text{ s}^{-1}$ . ( $k_{\text{cat}}/K_M$  determines the reaction rate at a very low concentration of a substrate when the enzyme is mostly free.) For comparison purposes, representative  $k_{\text{cat}}/K_M$  values for different esterases measured with pNPA have been reported, such as:  $2.3 \times 10^5 \text{ M}^{-1} \text{ s}^{-1}$ ,<sup>15</sup> and  $1.5 \times 10^4 \text{ M}^{-1} \text{ s}^{-1}$ ,<sup>16</sup> but recently also a much lower one of  $36 \text{ M}^{-1} \text{ s}^{-1}$ .<sup>17</sup> It is not clear if measured values using hydrolysis of pNPA have much relevance for comparison purposes to biological enzymes which are highly optimized for entirely different targets.

Detailed analysis by Rufo *et al.* showed that their peptides had to form large fibril aggregates having very high molecular weights for catalytic activity to occur. The fibrils formed by 11 were considerably more active than those reported by Pecoraro *et al.*, which also used zinc as a cofactor.<sup>18</sup> Peptide 11 was also comparably as effective as the most active one obtained by Kuhlman *et al.*<sup>19</sup>

To determine the effect of combining two peptides, 4 (Ac-LHLHLYL-CONH<sub>2</sub>,  $k_{\text{cat}}/K_M = 13 \text{ M}^{-1} \text{ s}^{-1}$ ) and 7 (Ac-LHLHLRL-CONH<sub>2</sub>,  $k_{\text{cat}}/K_M = 18 \text{ M}^{-1} \text{ s}^{-1}$ ) were first mixed in different proportions in aqueous HCl (to prevent formation of individual fibrils).<sup>7</sup> They were then diluted into  $\text{Zn}^{2+}$ -containing TRIS buffer at pH 8 and allowed to form

fibrils. A modest maximum catalytic effect was obtained at around 40% 4,  $k_{\text{cat}}/K_M \approx 23 \text{ M}^{-1} \text{ s}^{-1}$ .

Since 4 and 7 had identical sequences, except at position 6, and the key His were co-linear, it is not surprising that they did not interfere to form fibrils. However, mixing very different peptides able to form  $\beta$ -sheets individually would be expected to often interfere with fibril formation unless they were designed to interact together to form large  $\beta$ -sheets.

### Analysis of the results obtained

There are two reasons that this paper falls short of the claim in their title, “Short peptides self-assemble to produce catalytic amyloids” *in the context of a prebiotic environment*. The first is that the results are limited to special laboratory conditions. The second is a lack of relevance for amyloid world purposes.

### Results are restricted to special laboratory conditions.

The paper by Rufo *et al.*<sup>7</sup> is another example of the dramatic power of using *design* principles. Remarkably, this is a key characteristic of OoL research: *experts design and carry out experiments with a specific goal in mind*. Of  $20^7 = 1.28 \times 10^9$  potential heptapeptide sequences, only 14 were tested! Of the unfathomable number of possible chemical conditions (temperatures, pH, concentrations, cofactors, etc.) only those known in advance to offer the best opportunities had to be selected!

The team began with specific goals, namely designing peptides able to combine into  $\beta$ -sheets having ideally located His residues which could bind to  $\text{Zn}^{2+}$ . Naturalistic assumptions provided no guidance. For example, the key amino acid histidine would not have been present in measurable quantities on the putative prebiotic earth (nor any of the other ten amino acids they used shown in table 1, except for Ala, present in trace amounts).<sup>20,21</sup>

Their inspiration and key insights came from analyzing features of biological proteins, which clarified which residues should be used in which positions and with what cofactor.

Designer guidance is immediately recognized by the recurring need to chemically modify the terminal ends with stabilizing acetyl and carboxamide groups, which prevent hydrolysis, slow down racemization, and prevent interfering cross-reactions. Even the most effective catalyst they found, 11, was shown to lack activity entirely (within experiment error) when the cap groups were removed; see peptide 14 in table 1. Peptides 1–13 all consisted of 100% pure end-capped groups, eliminating all plausibility for OoL purposes.

Replacing just one H eliminated activity almost entirely as illustrated by comparing 9 and 12 in table 1. Recall that

**Table 1.** Heptapeptides examined and their catalytic effects in hydrolyzing p-nitrophenyl acetate. Data from Rufo *et al.*<sup>7</sup>

No.	Peptide	kcat/K <sub>M'</sub> M <sup>-1</sup> s <sup>-1</sup>	kcat×10 <sup>-2</sup> , s <sup>-1</sup>	B-sheets form at pH 8	Comments
1	Ac-LHLHLD-LCONH <sub>2</sub>	0.2 ± 0.1		Yes, only with Zn <sup>2+</sup>	Little / no activity: sidechain of D competes with H for zinc at positions 2 and 4.
2	Ac-LHLHLEL-CONH <sub>2</sub>	< 0.2		Yes, only with Zn <sup>2+</sup>	Little / no activity: sidechain of E competes with H for zinc at positions 2 and 4.
3	Ac-LHLHLQL-CONH <sub>2</sub>	30 ± 3		Yes, only with Zn <sup>2+</sup>	Q enhances forming amyloids, increased enzymatic effectiveness.
4	Ac-LHLHLYL-CONH <sub>2</sub>	13 ± 5		Yes	
5	Ac-LHLHLHL-CONH <sub>2</sub>	0.60 ± 0.08		Yes, even without Zn <sup>2+</sup>	Little / no activity: sidechain of Y competes with H for zinc at positions 2 and 4.
6	Ac-LHLHLKL-CONH <sub>2</sub>	12 ± 2		Yes, only with Zn <sup>2+</sup>	
7	Ac-LHLHLRL-CONH <sub>2</sub>	18 ± 4	3.2 ± 0.4	Yes, only with Zn <sup>2+</sup>	No activity in the absence of Zn <sup>2+</sup> .
8	Ac-AHAHARA-CONH <sub>2</sub>	0.12 ± 0.8		No	Replacing L → A in 7 to lower β-sheet propensity led to inactive an peptide.
9	Ac-IHIHIRI-CONH <sub>2</sub>	22 ± 8	4.2 ± 0.8	Yes, even without Zn <sup>2+</sup>	Replacing L → I in 7 to increase β-sheet propensity increased activity slightly.
10	Ac-VHVHVRV-CONH <sub>2</sub>	26 ± 4	3.8 ± 0.3	Yes, only with Zn <sup>2+</sup>	Replacing L → V in 7 to increase β-sheet propensity increased activity ~50%.
11	Ac-IHIHIQI-CONH <sub>2</sub>	62 ± 2	2.60 ± 0.04	Yes, even without Zn <sup>2+</sup>	Replacing R → Q of 9 in position 6 increased activity.
11a	Ac-VHVHVQV-CONH <sub>2</sub>	32 ± 2	1.6 ± 0.2	No data	Activity decrease by more than 100-fold without Zn <sup>2+</sup> .
12	Ac-IAIHIRI-CONH <sub>2</sub>	0.36 ± 0.16		Yes	Replacing one H in 9 eliminated activity almost entirely.
13	Ac-IHIAIRI-CONH <sub>2</sub>	0.2 ± 0.4		Yes	
14	H <sub>2</sub> N-IHIHIQI-COOH	1 ± 3		No	Removing acetyl and carboxamide groups from 11 eliminated activity.

no histidine would have been available in natural, prebiotic environments.

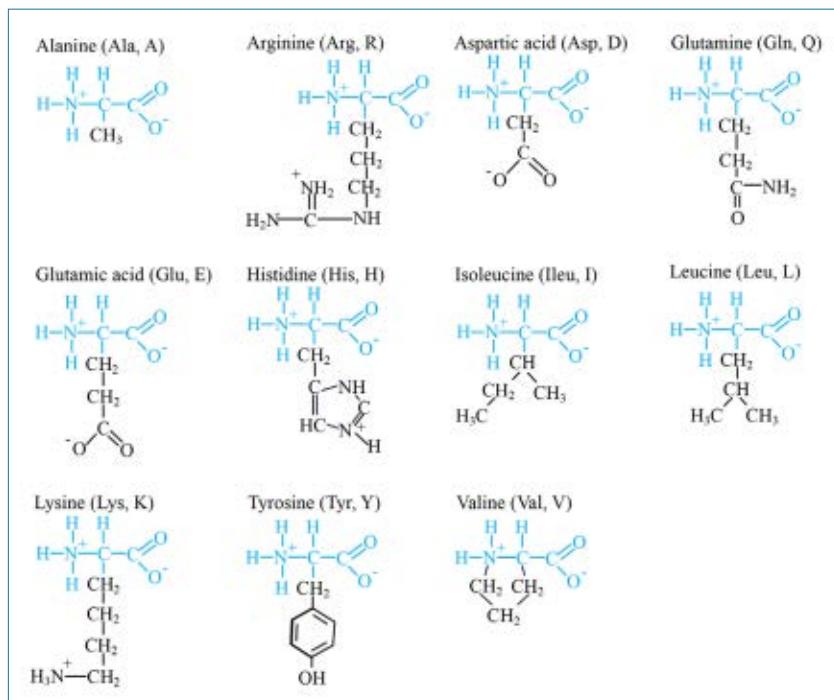
In addition, the presence of the cofactor Zn<sup>2+</sup> was of critical importance. The concentration of all soluble forms of zinc in oceans is about  $1 \times 10^{-9}$  M on average, which includes all forms of zinc, not only ZnCl<sub>2</sub>.<sup>22</sup> The concentration in the distant past would have been even lower, lacking industrial waste sources and erosional contribution from rivers over evolutionary billions of years. Of course, 100% of all oceanic Zn<sup>2+</sup> would not have been devoted to binding with these heptapeptides. However, the experiments used Zn<sup>2+</sup> concentration of  $1 \times 10^{-3}$  M, a million-fold higher concentration than available.

Rufo *et al.*<sup>7</sup> documented that catalytic activity was fairly constant at very high concentrations of Zn<sup>2+</sup> but then dropped linearly with decreasing Zn<sup>2+</sup>, starting from a stoichiometry

of ~1:2 (zinc to peptide), as shown by the red dotted line in figure 3. The 1:2 stoichiometry implied that one Zn<sup>2+</sup> bound with two peptides, as designed.

The hydrolysis of pNPA shown in figure 3 was catalyzed by a concentration of  $24 \times 10^{-6}$  M peptide, and ~80% of the maximum activity required a stoichiometry of at least 1:2 zinc to peptide. However, taking the available concentration of zinc into account reveals that in a credible prebiotic scenario less than 1 / 10,000 of the peptide pairs could have been bound to a Zn<sup>2+</sup>. The result of having essentially no cofactor would have been no catalytic effect. Living organisms have complex biological sensors and transporters able to import zinc from the environment, but synthesized fibrils don't.<sup>23,24</sup>

Of course, one could lower the concentration of peptide to ensure binding to a Zn<sup>2+</sup>. But concentrations of ~ $1 \times 10^{-9}$



**Figure 2.** Structures of the amino acids used in the peptides studied. The regions forming a linear peptide backbone are shown in blue and the sidechains in black.

M for both peptide and zinc would not form fibrils at a rate relevant to OoL purposes, and even if they somehow had protecting capping groups, hydrolysis and racemization would have destroyed the peptides over immense time periods.

A concentration of 24  $\mu\text{M}$  pure peptide, seven residues long, would not have formed naturally in water. No OoL research has reported linear, homochiral heptapeptides forming under credible aqueous prebiotic conditions, far less so devoid of glycine residues. Note that the family of peptides designed by Rufo *et al.* would also have needed to contain two His and other complex amino acids. As documented in figure 2, of all the amino acids used by Rufo *et al.*, only three contained unreactive alkyl sidechains. The experimental setup had to avoid all interfering sidechain reactions in addition to reactions with interfering carboxylic acids, amines, and non-biological amino acids found in the environment.

These problems were avoided by synthesizing the peptides using a complex fluorenylmethyloxycarbonyl (Fmoc) protocol at elevated temperature using the solvents trifluoroacetic acid and triisopropyl silane.<sup>25</sup> The technique involved first protecting the sidechains chemically and then freeing them with a different chemical reaction.

The authors pointed out correctly that enzymes usually require  $>100$  residues to form a reliable, stable folded

structure. Searching through this space of possibilities to find useful enzymes would not be feasible by chance. But neither is it realistic to require hundreds or thousands of almost identical pure peptides with just the right sequences to be concentrated at the same location to form fibrils joined pairwise by (non-existent)  $\text{Zn}^{2+}$  ions.

Finally, we must not overlook that the hydrolysis reaction involved pNPA, a tiny molecule presumably capable of easily accessing the catalytic site of the fibrils. No experiments were reported about the ability of the designed fibrils to hydrolyze much larger relevant biochemicals. Certainly, they could not perform a vital function of many enzymes: the *coupling* of energetically favourable to unfavourable reactions.

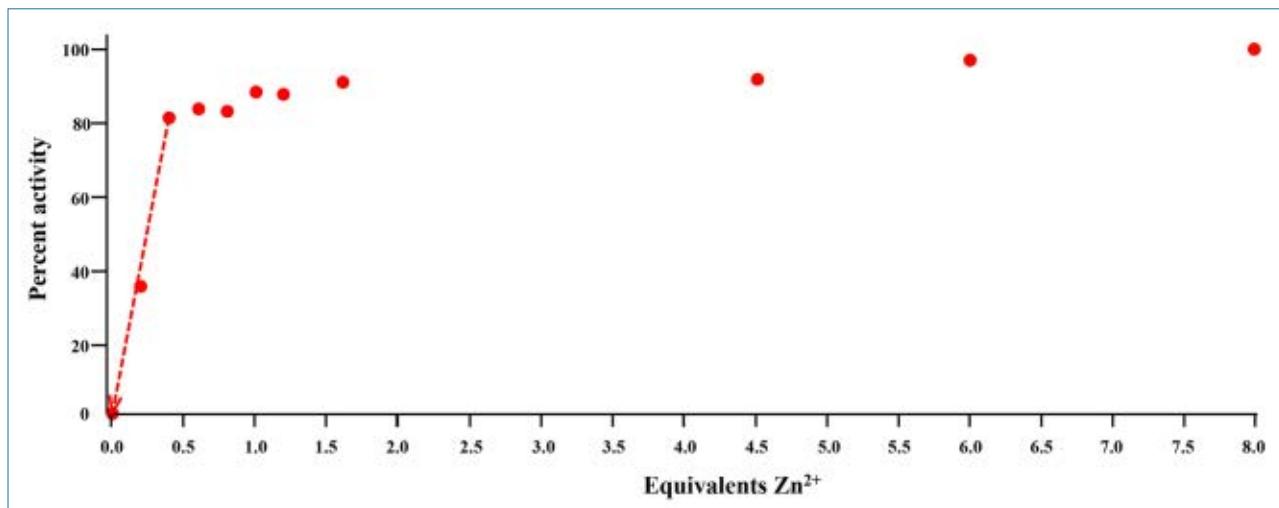
### Lack of relevance for Amyloid World Hypothesis purposes

Suppose that these kinds of amyloid fibrils could have formed under prebiotic-type conditions which facilitated hydrolysis of amide, ester, lipid, and many other classes of molecules. However, what OoL researchers require are not substances able to *randomly hydrolyze molecules needed for their prebiotic models but rather mechanisms to increase their sizes* to produce huge protein, RNA, and DNA sequences.

It is important not to overlook that no method was proposed to select what is to be hydrolyzed nor when or where. *Regulation like this is indispensable for enzymes* and all life-related chemical processes.

Unfortunately, the authors did not mix short RNA and DNA strands to their fibrils for long time periods under different conditions to determine if they would be catalytically destroyed. This is an example of how only the experiments able to support the naturalist agenda are designed and published.<sup>26</sup> This creates the often-repeated illusion that “tons of research papers support that abiogenesis is a fact”.<sup>27</sup>

Unlike *highly specific* biological enzymes, the fibril aggregates described would be indiscriminate of the hydrolyzable molecule it encountered. How this work would support the Amyloid World Hypothesis is a mystery. Were the fibrils fairly homogenous ‘organisms’ which hydrolyzed some molecules, or would a multitude of different fibril aggregates have been needed that collaborated as an ‘organism’ to hydrolyze a wider variety of organic molecules? Notice that



**Figure 3.** Catalytic activity of peptide 11 (Ac-IHIHQI-CONH<sub>2</sub>) as a function of Zn<sup>2+</sup> concentration. Activity increased linearly from no zinc until a stoichiometry of ~1:2 zinc to peptide, then levelled off. (Redrawn with small alterations from fig. 2c of Rufo *et al.*<sup>7</sup>)

even the acetyl end cap of the peptides would be, in theory, at risk of being catalysed.

Biological proteins are not characterized by amphipathic sequences, and there is no evidence they arose from these kinds of amyloids.

### Conclusions and take-home messages

Rufo *et al.* provided a well-written paper that illustrated the highly effective manner in which chemists go about identifying goals and then designing efficient pathways to achieve them. These are fundamental skills chemists learn. A variety of sophisticated techniques were expertly applied, but the experimental conditions were not relevant for a theoretical prebiotic world.

- The heptapeptides were carefully designed based on insights from biological zinc-binding esterases. Unique homochiral sequences were designed that could form extended β-sheets and bind to Zn<sup>2+</sup>.
- The experimental goal-oriented strategy and incorporation of insights gained to obtain better catalysts is an excellent example of how intelligence can rapidly produce results inconceivable through unguided, natural processes.
- To obtain a catalytic effect, large fibril aggregates had to form consisting of hundreds or thousands of pure, nearly identical heptapeptides.
- Of the ten amino acids used to construct this family of peptides, nine are not expected to have existed in a prebiotic world, in particular the key histidine residues which formed the foundation of these experiments.
- The fibril-forming peptides all had to be chemically modified to acetyl and carboxamide groups, which eliminated all relevance to prebiotic conditions. No catalytic effect

resulted (within experimental error) when the end-caps were removed.

- Replacing just one histidine eliminated almost all catalytic power.
- Pure heptapeptides were used in an unrealistic concentration of 24 μM. Homochiral, linear peptides this length which lack glycine residues have not been reported in any OoL experiments under any plausible conditions (far less aqueous solutions).
- Seven of the ten amino acids used in the experiments have potentially reactive side chains. This problem, plus the need for long, homochiral peptides, was resolved by manually synthesizing all the peptides in a laboratory, complete with end-capping, and then chemically removing the side-chain-protecting groups once the peptides had been constructed.
- The catalytic effect depended on Zn<sup>2+</sup> as a cofactor and a concentration of  $1 \times 10^{-3}$  M was used, whereas the concentration found in oceans is  $\sim 1 \times 10^{-9}$  M. If all zinc available in oceans had been devoted only to forming this family of heptapeptides, a maximum concentration of  $\sim 1 \times 10^{-9}$  M peptide could have been bound to Zn<sup>2+</sup>. Figure 3 shows how no discernible catalytic effect would have resulted.
- Maximum concentration of heptapeptides and Zn<sup>2+</sup> of about 1 nM each would not have formed fibrils in any measurable concentration, far less in concentrations and amounts relevant to support an amyloid world.
- What OoL researchers require to support an Amyloid World Hypothesis are not substances able to indiscriminately hydrolyze molecules but rather mechanisms to increase the sizes of life-relevant polymers, such as proteins, RNAs, and DNAs.

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27. This claim is made by several atheist YouTubers with hypnotizing frequency.

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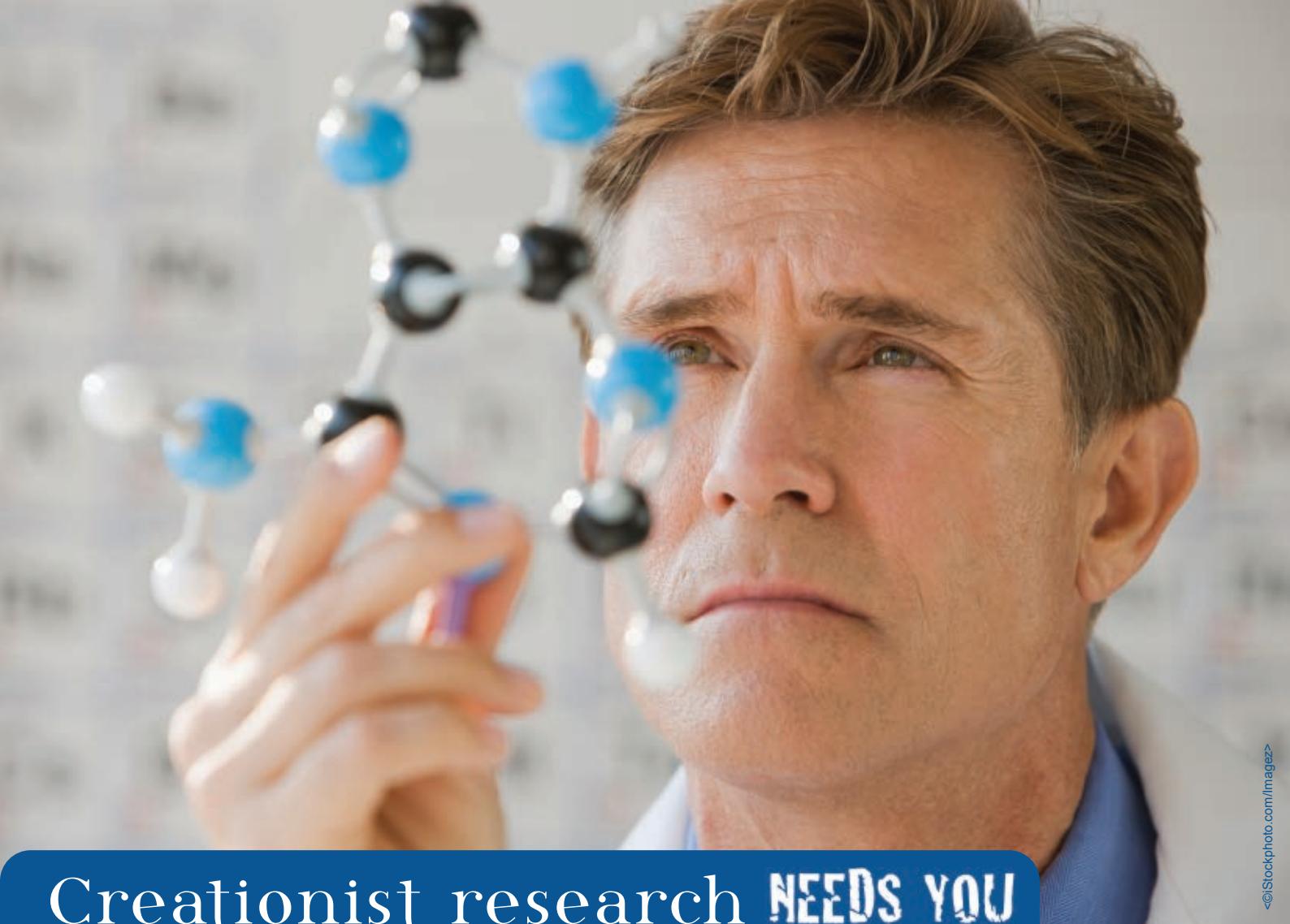
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